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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 75.4483 Seconds  
(without alignments)  
520,498 Million cell updates/sec

Title: US-10-007-255-9  
Perfect score: 1 cttatcagacacgtcttcaaga 24  
Sequence: 4

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	568	2	US-08-439-814-4
2	24	100.0	1318	2	US-08-439-814-3
3	24	100.0	1688	2	US-08-439-814-2
4	24	100.0	2090	2	US-08-439-814-1
5	17.2	71.7	601	4	US-09-949-016-70889
6	17.2	71.7	601	4	US-09-949-016-70890
7	17.2	71.7	13204	4	US-09-054-227-49
8	17.2	71.7	125536	4	US-09-949-016-14186
9	17.2	71.7	276687	4	US-09-949-016-13840
10	17	70.8	92	4	US-09-621-976-17501
11	17	70.8	103	4	US-09-621-976-17501
12	17	70.8	136	4	US-09-621-976-17503
13	17	70.8	137	4	US-09-621-976-17502
14	17	70.8	150	4	US-09-621-976-13989
15	17	70.8	169	4	US-09-621-976-11249
16	17	70.8	179	4	US-09-621-976-9575
17	16.8	70.0	26313	4	US-09-949-016-16117
18	16.8	70.0	81384	4	US-09-949-016-12422
19	16.6	69.2	406	4	US-09-621-976-14718
20	16.6	69.2	601	4	US-09-949-016-29459
21	16.6	69.2	601	4	US-09-949-016-15385
22	16.6	69.2	601	4	US-09-949-016-18573
23	16.6	69.2	601	4	US-09-949-016-19508
24	16.6	69.2	601	4	US-09-949-016-19508
25	16.6	69.2	1572	4	US-09-107-532A-495
26	16.6	69.2	24847	4	US-09-949-016-16056
27	16.6	69.2	25464	4	US-09-326-480A-4

28	16.6	69.2	28696	4	US-09-949-016-17054	Sequence 17054, A
29	16.6	69.2	28780	4	US-09-949-016-12335	Sequence 12335, A
30	16.6	69.2	40130	4	US-09-949-016-17275	Sequence 17275, A
31	16.6	69.2	142504	4	US-09-949-016-13693	Sequence 13693, A
32	16.6	69.2	142506	4	US-09-949-016-12474	Sequence 12474, A
33	16.6	69.2	248968	4	US-09-949-016-12614	Sequence 12614, A
34	16.6	69.2	250958	4	US-09-949-016-16061	Sequence 16061, A
35	16.6	69.2	260266	4	US-09-949-016-17037	Sequence 17037, A
36	16.6	69.2	260293	4	US-09-949-016-12106	Sequence 12106, A
37	16.6	69.2	1330121	4	US-09-557-884-1	Sequence 1, Appl
38	16.6	69.2	1330121	4	US-09-643-990A-1	Sequence 1, Appl
39	16.2	67.5	856	4	US-09-308-080-7	Sequence 7, Appl
40	16.2	67.5	861	4	US-09-308-080-1	Sequence 19, Appl
41	16.2	67.5	1503	4	US-09-184-418C-29	Sequence 29, Appl
42	16.2	67.5	8953	4	US-09-184-418C-3	Sequence 3, Appl
43	16.2	67.5	41755	4	US-09-949-016-15728	Sequence 15728, A
44	16.2	67.5	200663	4	US-09-949-016-12569	Sequence 12569, A
45	16.2	67.5	203093	4	US-09-949-016-14445	Sequence 14445, A

## ALIGNMENTS

RESULT 1  
US-08-439-814-4/c  
Sequence 4, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:  
APPLICANT: STEIN, Ulrike  
APPLICANT: WALTHER, Wolfgang  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
TITLE OF INVENTION: THERAPY-RELEVANT GENES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARNELESTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
STREET: Street Lobby  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439, 814  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE93/01086

FILED DATE: 10-NOV-1993  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 568 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-439-814-4

Query Match 100.0%; Score 24; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTCAAG 24  
DB 203 CTTATGTAGACAGCTTTCAAG 180

RESULT 2  
US-08-439-814-3/c  
Sequence 3, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:  
APPLICANT: STEIN, Uli-ke  
APPLICANT: WALTHER, Wolfgang  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKALDO, NARMELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,814  
CLASSIFICATION: 514  
FILING DATE: 12-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1318 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-439-814-3

Query Match 100.0%; Score 24; DB 2; Length 1318;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTCAAG 24  
DB 953 CTTATGTAGACAGCTTTCAAG 930

RESULT 3  
US-08-439-814-2/c  
Sequence 2, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:  
APPLICANT: STEIN, Uli-ke  
APPLICANT: WALTHER, Wolfgang  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKALDO, NARMELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,814  
CLASSIFICATION: 514  
FILING DATE: 12-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1688 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)



US-06-439-814-2

Query Match 100.0%; Score 24; DB 2; Length 1688;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTATGTAGACAGCTTTCAAG 24  
DB 1323 CTTATGTAGACAGCTTTCAAG 1300

RESULT 4

US-06-439-814-1/C  
Sequence 1, Application US/06439814

Patent No. 5968735

GENERAL INFORMATION:

APPLICANT: STEIN, Ulrike

TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

STREET: 655 Fifteenth Street, N. W., Suite 330 G

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/06/439, 814

FILING DATE: 12-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 4238778.7

FILING DATE: 12-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE PCT/DE93/01086

FILING DATE: 10-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: KLESNER, Sharon N.

REGISTRATION NUMBER: 36,335

REFERENCE/DOCKET NUMBER: P1614-5015

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTATGTAGACAGCTTTCAAG 24  
DB 1725 CTTATGTAGACAGCTTTCAAG 1702

RESULT 5

US-09-949-016-70889/C  
Sequence 70889, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 70889

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-70889

Query Match 71.7%; Score 17.2; DB 4; Length 601;

Best Local Similarity 86.4%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTATGTAGACAGCTTTCAAA 23  
DB 315 TTATGTATACATGCTTTTAA 294

RESULT 6

US-09-949-016-70890/C  
Sequence 70890, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 70890

LENGTH: 601

TYPE: DNA

ORGANISM: Human

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTATGTAGACAGCTTTCAAA 23  
DB 95 TTATGTATACATGCTTTTAA 74

RESULT 7

US-09-949-016-70890/C  
Sequence 70890, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 70890

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-70890

Query Match 71.7%; Score 17.2; DB 4; Length 601;

Best Local Similarity 86.4%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7  
US-09-054-272-49  
Sequence 49, Application US/09054272  
Patent No. 6692909  
GENERAL INFORMATION:  
APPLICANT: Lander, Eric S.  
APPLICANT: Daley, George O.  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Rozen, Steven G.  
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS  
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054,272  
FILING DATE: 01-APR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WHI98-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13204 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-054-272-49

Query Match 71.7%; Score 17.2; DB 4; Length 13204;  
Best Local Similarity 86.4%; Pred. No. 1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCTTCA 22  
DB 4230 CTAATGTAGACAGCTCTTCA 4251

RESULT 8  
US-09-949-016-14186/c  
Sequence 14186, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14186  
LENGTH: 125536  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-14186

Query Match 71.7%; Score 17.2; DB 4; Length 125536;  
Best Local Similarity 86.4%; Pred. No. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACAGCTCTTCA 23  
DB 120935 TTATGAAGACAGCTCTTAA 120914

RESULT 9  
US-09-949-016-13840/c  
Sequence 13840, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13840  
LENGTH: 276687  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(276687)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13840

Query Match 71.7%; Score 17.2; DB 4; Length 276687;  
Best Local Similarity 86.4%; Pred. No. 1.7e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACAGCTCTTCA 23  
DB 43890 TTATGTATACATGCTTTAA 43869

RESULT 10  
US-09-621-976-17500/c  
Sequence 17500, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Robert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm

SEQ ID NO 17500  
LENGTH: 92  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-621-976-17500

Query Match 70.8%; Score 17; DB 4; Length 92;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17  
|||||  
DB 74 CTTATGTAGACAGCTCT 58

RESULT 11  
US-09-621-976-17501/c  
Sequence 17501, Application US/09621976  
Patent No. 6639063

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 17501  
LENGTH: 103  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-621-976-17501

Query Match 70.8%; Score 17; DB 4; Length 103;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17  
|||||  
DB 74 CTTATGTAGACAGCTCT 58

RESULT 12  
US-09-621-976-17503/c  
Sequence 17503, Application US/09621976  
Patent No. 6639063

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 17503  
LENGTH: 126  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-621-976-17503

Query Match 70.8%; Score 17; DB 4; Length 126;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17  
|||||  
DB 74 CTTATGTAGACAGCTCT 58

RESULT 13

US-09-621-976-17502/c  
Sequence 17502, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 17502  
LENGTH: 137  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-621-976-17502

Query Match 70.8%; Score 17; DB 4; Length 137;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17  
|||||  
DB 74 CTTATGTAGACAGCTCT 58

RESULT 14  
US-09-621-976-13989/c  
Sequence 13989, Application US/09621976  
Patent No. 6639063

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 13989  
LENGTH: 150  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-621-976-13989

Query Match 70.8%; Score 17; DB 4; Length 150;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17  
|||||  
DB 74 CTTATGTAGACAGCTCT 58

RESULT 15  
US-09-621-976-11249/c  
Sequence 11249, Application US/09621976  
Patent No. 6639063

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 11249

/ LENGTH: 169  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 169  
 / OTHER INFORMATION: n=a, 5, c or t  
 US-09-621-976-11249

Query Match 70.8%; Score 17, DB 4, Length 169;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Qy 1 CTTATGTAGACACGTCT 17  
 |||||  
 Db 74 CTTATGTAGACACGTCT 58

Search completed: February 9, 2005, 17:11:13  
 Job time : 79.4483 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 256 Seconds  
(without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-9

Perfect score: 24  
Sequence: 1 cttatgtagacacgcttcaag 24

Scoring table: IDENTITY NUC  
Gapop 10'-0, Gapext 1.0

Searched: 431806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	24	100.0	633	18	US-10-482-433A-3
2	24	100.0	2932	18	US-10-473-126-37
3	19.8	82.5	633	18	US-10-482-433A-6
4	19.8	82.5	2932	17	US-10-451-646-24
5	19.8	82.5	2932	18	US-10-473-126-167
6	18.2	75.8	491	18	US-09-770-961-577
7	18.2	75.8	494	10	US-10-357-930-19156
8	18.2	75.8	520	18	US-10-357-930-19156
9	18.2	75.8	597	18	US-10-357-930-54995
10	18.2	75.8	642	18	US-10-357-930-48960
11	18.2	75.8	1504	18	US-10-437-963-86301

12	18.2	75.8	2932	18	US-10-473-126-168	Sequence 168, App
13	18.2	75.8	2932	18	US-10-473-126-313	Sequence 313, App
14	17.8	74.2	619	13	US-10-027-633-8632	Sequence 8632, Ap
15	17.8	74.2	619	17	US-10-027-633-8632	Sequence 8632, Ap
16	17.8	74.2	665	13	US-10-027-633-99405	Sequence 99405, A
17	17.8	74.2	665	13	US-10-027-633-99406	Sequence 99406, A
18	17.8	74.2	665	17	US-10-027-633-99405	Sequence 99405, A
19	17.8	74.2	665	17	US-10-027-633-99406	Sequence 99406, A
20	17.8	74.2	665	17	US-10-027-633-99406	Sequence 99406, A
21	17.8	74.2	303172	18	US-10-719-993-6890	Sequence 6890, Ap
22	17.6	73.3	277	10	US-09-814-353-5277	Sequence 5277, Ap
23	17.6	73.3	277	10	US-09-814-353-12011	Sequence 12011, A
24	17.6	73.3	340	18	US-10-357-930-50147	Sequence 50147, A
25	17.4	72.5	1353	13	US-10-282-122A-38309	Sequence 38309, A
26	17.4	72.5	201	18	US-10-741-601-19969	Sequence 19969, A
27	17.4	72.5	61177	18	US-10-741-601-5694	Sequence 5694, Ap
28	17.2	71.7	25	15	US-10-098-263B-45459	Sequence 45459, A
29	17.2	71.7	159	15	US-10-097-111-147	Sequence 147, App
30	17.2	71.7	392	18	US-10-674-124A-13252	Sequence 13252, A
31	17.2	71.7	633	13	US-10-027-633-274931	Sequence 274931, A
32	17.2	71.7	633	13	US-10-027-633-274932	Sequence 274932, A
33	17.2	71.7	633	17	US-10-027-633-274931	Sequence 274931, A
34	17.2	71.7	780	18	US-10-437-963-23635	Sequence 23635, A
35	17.2	71.7	840	15	US-10-097-111-1	Sequence 1, Appl
36	17.2	71.7	869	17	US-10-425-114-10735	Sequence 10735, A
37	17.2	71.7	1067	17	US-10-424-599-35770	Sequence 35770, A
38	17.2	71.7	1446	17	US-10-282-122A-18304	Sequence 18304, A
39	17.2	71.7	15783	10	US-09-764-872-700	Sequence 700, App
40	17.2	71.7	28953	18	US-10-719-993-6811	Sequence 6811, Ap
41	17.2	71.7	56506	15	US-10-097-111-10	Sequence 10, Appl
42	17.2	70.8	342	9	US-09-864-761-6452	Sequence 6452, Ap
43	16.8	70.0	635	13	US-10-637-855-398	Sequence 398, App
44	16.8	70.0	635	13	US-10-027-632-214760	Sequence 214760, A
45	16.8	70.0	635	13	US-10-027-632-214761	Sequence 214761, A

#### ALIGNMENTS

RESULT 1  
US-10-482-433A-3/c  
; Sequence 3, Application US/10482433A  
; Publication No. US20040265814A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative  
; FILE REFERENCE: 82174  
; CURRENT FILING DATE: 2003-12-29  
; PRIOR APPLICATION NUMBER: DE 10132212.7  
; PRIORITY FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 633  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amplification Product of MdRI-Fragment  
US-10-482-433A-3

Query Match 100.0%; Score 24; DB 18; Length 633;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTCAAG 24  
|||||  
DB 211 CTTATGTAGACACGCTTCAAG 188

RESULT 2  
US-10-473-126-37/c

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Sequence 37, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 37
LENGTH: 2932
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-473-126-37
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 2932;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTTTTCAAA 24
DB 828 CTTATGTAGACACGCTTTTCAAA 805
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```
RESULT 3
US-10-482-433A-6/c
Sequence 6, Application US/10482433A
Publication No. US20040265814A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative
FILE REFERENCE: 82174
CURRENT APPLICATION NUMBER: US/10/482,433A
CURRENT FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: DE 10132212.7
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 633
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amplification Product Of Bisulfite-Treated DNA
US-10-482-433A-6
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```
Query Match
Best Local Similarity 82.5%; Score 19.8; DB 18; Length 633;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTTTTCAAA 23
DB 211 CTTATATATAACACGCTTTTCAAA 189
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```
RESULT 4
US-10-451-646-24/c
Sequence 24, Application US/10451646
Publication No. US20040067508A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method for the Simultaneous Amplification of Multiple
FILE REFERENCE: PCT/DE 01/04951
CURRENT APPLICATION NUMBER: US/10/451,646
CURRENT FILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 2932
TYPE: DNA
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: bisulphite treated sequence
US-10-451-646-24
```

```
Query Match
Best Local Similarity 82.5%; Score 19.8; DB 17; Length 2932;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTTTTCAAA 23
DB 828 CTTATATATAACACGCTTTTCAAA 806
```

```
RESULT 5
US-10-473-126-167/c
Sequence 167, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 167
LENGTH: 2932
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-167
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```
Query Match
Best Local Similarity 82.5%; Score 19.8; DB 18; Length 2932;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTTTTCAAA 23
DB 828 CTTATATATAACACGCTTTTCAAA 806
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```
RESULT 6
US-10-437-963-86300
Sequence 86300, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 86300
LENGTH: 491
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(491)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_85354C.1
US-10-437-963-86300
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Query Match 75.8%; Score 18.2; DB 18; Length 491;  
Best Local Similarity 87.0%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTATGTAGACGCTTTCAAG 24  
DB 53 TTATGTAGACGCTTTCAAG 75

## RESULT 7

US-09-770-961-577/C  
; Sequence 577, Application US/09770961  
; Publication No. US20030115639A1  
; GENERAL INFORMATION:  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameake, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Mathew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Moesner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; TITLE OF INVENTION: thaliana  
; FILE REFERENCE: 2026 (PARR-015PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,961  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,466  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 577  
; LENGTH: 494  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-961-577

Query Match 75.8%; Score 18.2; DB 10; Length 494;  
Best Local Similarity 87.0%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTATGTAGACGCTTTCAAG 24  
DB 297 TTATGTAGACGCTTTCAAG 275

## RESULT 8

US-10-357-930-19156  
; Sequence 19156, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endege, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276

; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19156  
; LENGTH: 520  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 166..171  
; OTHER INFORMATION: n = A,T,C or G

US-10-357-930-19156

Query Match 75.8%; Score 18.2; DB 18; Length 520;  
Best Local Similarity 87.0%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTTATGTAGACGCTTTCAAA 23  
DB 303 CTTATGTAGACGCTTTCAAA 325

## RESULT 9

US-10-357-930-54995/C  
; Sequence 54995, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endege, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 54995  
; LENGTH: 597  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-357-930-54995

Query Match 75.8%; Score 18.2; DB 18; Length 597;  
Best Local Similarity 87.0%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTCAAA 23  
|||  
Db 142 CTTATGTAGATATGCTTTTCAAA 120

RESULT 10  
US-10-357-930-48960  
; Sequence 48960, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endesig, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48960  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-357-930-48960

Query Match 75.8%; Score 18.2; DB 18; Length 642;  
Best Local Similarity 87.0%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CTTATGTAGACACGCTTTCAAA 23  
|||  
Db 372 CTTATGTAGACTCTTTTCAAA 394

RESULT 11  
US-10-437-963-86301  
; Sequence 86301, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 86301  
; LENGTH: 1504  
; TYPE: DNA

ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_85355C.1  
US-10-437-963-86301

Query Match 75.8%; Score 18.2; DB 18; Length 1504;  
Best Local Similarity 87.0%; Pred. No. 1.5e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TTATGTAGACACGCTTTCAAG 24  
|||  
Db 189 TTATGTAGATATGCTTTCAAG 211

RESULT 12  
US-10-473-126-168  
; Sequence 168, Application US/10473126  
; Publication No. US20040234973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; FILE REFERENCE: proliferative disorders  
; CURRENT APPLICATION NUMBER: US/10/473,126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 168  
; LENGTH: 2932  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-473-126-168

Query Match 75.8%; Score 18.2; DB 18; Length 2932;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TTATGTAGACACGCTTTCAAG 24  
|||  
Db 2106 TTATGTAGATATGCTTTTAAAG 2128

RESULT 13  
US-10-473-126-313/C  
; Sequence 313, Application US/10473126  
; Publication No. US20040234973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; FILE REFERENCE: proliferative disorders  
; CURRENT APPLICATION NUMBER: US/10/473,126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 313  
; LENGTH: 2932  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-473-126-313

Query Match 75.8%; Score 18.2; DB 18; Length 2932;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CTTATGTAGACACGCTTTCAAA 23  
|||  
Db 828 CTTATATTAACATCTTTCAAA 806

RESULT 14



```

US-10-027-632-8632
; Sequence 8632, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.139
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8632
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-8632

```

Ox	3	TATGTAGACAGCTCTTCAAA	23
Db	523	TATAGACAGCTGTTCAAA	543

Best Match 74.2% Score 17.8; DB 17; Length 619;  
 Query Similarity 90.5% Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01, Search time 235.862 Seconds  
(without alignments)  
602.360 Million cell updates/sec

Title: US-10-007-255-9  
Perfect score: 24  
Sequence: 1 ctatcgtacacgccttcctcaag 24

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: N\_Geneseq\_16Dec04:\*  
1: geneeqn19808:\*  
2: geneeqn19908:\*  
3: geneeqn20008:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	24	6 AAD39008	Aad39008 Human mdr
C 2	24	100.0	24	6 AAD38998	Aad38998 Human mdr
C 3	24	100.0	568	2 AAG62615	Aag62615 Human mdr
C 4	24	100.0	633	8 ABX94595	Abx94595 Human mdr
C 5	24	100.0	1318	2 AAG62614	Aag62614 Human mdr
C 6	24	100.0	1688	2 AAG62613	Aag62613 Human mdr
C 7	24	100.0	2090	2 AAG62612	Aag62612 Human mdr
C 8	24	100.0	2932	10 ABE209897	Ab209897 Human 5'
C 9	24	100.0	2932	10 ADE84005	Ad84005 5' regula
C 10	24	100.0	2932	13 ADE84005	Ad84005 Human ABC
C 11	24	100.0	2932	13 ADE84005	Ad84005 Human ABC
C 12	24	100.0	8573	6 ABE98184	Ab98184 Human mdr
C 13	24	100.0	10200	6 AAD41243	Aad41243 Human mdr
C 14	24	100.0	177380	8 ACF62751	Ac62751 Cancer ba
C 15	24	100.0	177380	8 ADB20870	Ad20870 MRP1 base
C 16	24	100.0	177380	10 ADB87959	Ad87959 Human UGT
C 17	24	100.0	177380	10 ADB96942	Ad96942 Human MDR
C 18	24	100.0	177380	10 ADB92133	Ad92133 Human mdr
C 19	23	95.8	23	6 AAD39037	Aad39037 Human mdr
C 20	23	95.8	23	6 AAD39033	Aad39033 Human mdr

C 21	22	91.7	22	6 AAD39034	Aad39034 Human mdr
C 22	22	91.7	22	6 AAD39038	Aad39038 Human mdr
C 23	21	87.5	21	6 AAD39035	Aad39035 Human mdr
C 24	21	87.5	21	6 AAD39039	Aad39039 Human mdr
C 25	20	83.3	20	6 AAD39040	Aad39040 Human mdr
C 26	19.8	82.5	633	8 ABX94598	Abx94598 Human mdr
C 27	19.8	82.5	2932	6 ABE85526	Ab85526 Human bis
C 28	19.8	82.5	2932	8 ABE210027	Ab210027 Haematopo
C 29	19.8	82.5	2932	10 ADB54077	Ad54077 Pretreat
C 30	19.8	82.5	2932	10 ADB84065	Ad84065 Human lym
C 31	19.8	82.5	2932	13 ADE89231	Ad89231 Oligonuc
C 32	19	79.2	19	4 AAF91153	Aaf91153 Human mul
C 33	19	79.2	19	4 AAF91155	Aaf91155 Human mul
C 34	18.8	78.3	650	4 AAF88286	Aaf88286 H. tuberc
C 35	18.6	77.5	19	4 AAF91154	Aaf91154 Human mul
C 36	18.6	77.5	19	4 AAF91156	Aaf91156 Human mul
C 37	18.6	77.5	19	8 ACF62678	Ac62678 Cancer ba
C 38	18.6	77.5	19	8 ACF62678	Ac62678 Cancer ba
C 39	18.6	77.5	19	8 ADB21349	Ad21349 MRP1 base
C 40	18.6	77.5	19	8 ADB21350	Ad21350 MRP1 base
C 41	18.6	77.5	19	10 ADB88438	Ad88438 Human UGT
C 42	18.6	77.5	19	10 ADB88439	Ad88439 Human UGT
C 43	18.6	77.5	19	10 ADB87421	Ad87421 Human MDR
C 44	18.6	77.5	19	10 ADB97422	Ad97422 Human MDR
C 45	18.6	77.5	19	10 ADB92613	Ad92613 Human MDR

## ALIGNMENTS

RESULT 1	AAD39008/c	AAD39008 standard; DNA; 24 BP.
ID	AAD39008	
AC	AAD39008	
XX		
DT	23-SEP-2002	(first entry)
XX		
DE	Human mdr1 gene HIF-1 binding site DNA #1.	
XX		
XX	Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;	
KW	lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;	
KW	myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;	
KW	angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;	
KW	polycythaemia vera; hypoxia responsive element; HRE; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	misc_binding	10..14
FT		/*tag= a
FT		/bound_molecly= "HIF-1"
XX		
XX	WO200234291-A2.	
XX	02-MAY-2002.	
PD		
XX	25-OCT-2001; 2001WO-US049856.	
XX	26-OCT-2000; 2000US-0243542P.	
XX	(BGHM ) BRIGHAM & WOMENS HOSPITAL INC.	
XX	Colgan SP;	
XX	WPI; 2002-471427/50.	
DR		
XX	Treating a subject (at risk of) having a hematologic malignancy or	
XX	multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia	
PT	inducible factor 1 binding molecules or small ubiquitin-like-modifier-1	
PT	binding molecules.	
XX		

PS Example 2; Page 12; 92pp; English.  
XX  
CC The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC (e.g. lymphoma, myeloma or chronic lymphocytic leukaemia). The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is human mdr1  
CC gene HIF-1 binding site DNA  
SQ  
Sequence 24 BP; 8 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.085;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTATGTAGACACGCTTTCAAG 24  
Db 24 CTTATGTAGACACGCTTTCAAG 1  
RESULT 2  
AAD38998  
ID AAD38998 standard; DNA; 24 BP.  
XX  
AC AAD38998;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human mdr1-HRE antisense oligonucleotide #1.  
XX  
KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;  
KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;  
KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;  
KW angiotenic myeloid metaplasia; myeloid leukaemia; gene therapy;  
KW polycythaemia vera; hypoxia responsive element; HRE; antisense;  
KW phosphorothioate backbone; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT 1..24 /\*tag= a  
FT modified\_base /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
PN W0200234291-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 25-OCT-2001; 2001WO-US049856.  
XX  
PR 26-OCT-2000; 2000US-0243542P.  
XX  
PA (BGM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX  
PI Colgan SP;  
XX  
WI WPI; 2002-471427/50.  
XX  
PT Treating a subject (at risk of) having a hematologic malignancy or  
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia  
PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT binding molecules.  
XX  
PS Claim 14; Page 43; 92pp; English.  
XX  
CC The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC (e.g. lymphoma, myeloma or chronic lymphocytic leukaemia). The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is an antisense  
CC oligo targeted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its  
CC expression. This oligo is used in the exemplification of the invention  
XX  
SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.085;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTATGTAGACACGCTTTCAAG 24  
Db 1 CTTATGTAGACACGCTTTCAAG 24  
RESULT 3  
AAQ62615/C  
ID AAQ62615 standard; DNA; 568 BP.  
XX  
AC AAQ62615;  
XX  
DT 25-MAR-2003 (revised)  
DT 17-JAN-1995 (first entry)  
XX  
DE Human mdr-1 promoter fragment.  
XX  
KW Inducible promoter; cytostatic agent; adriamycin; vincristine;  
KW multiple drug resistance; mdr-1; mammalian expression vector;  
KW cancer therapy; ss.  
XX  
OS Homo sapiens.  
OS  
XX  
PN DE4238778-A1.  
XX  
PD 19-MAY-1994.  
XX  
PF 12-NOV-1992; 92DE-04238778.  
XX  
PR 12-NOV-1992; 92DE-04238778.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Stein U, Walthers W;  
XX  
WI WPI; 1994-168680/21.  
XX  
PT New mammalian expression vector useful for gene therapy, - comprising the  
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to  
PT cytostatic agents.  
XX  
PS Claim 2; Page 6; 7pp; German.  
XX  
CC This is a preferred fragment of the mdr-1 gene promoter, isolated from  
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by  
CC cytostatic agents such as vincristine and adriamycin which are used in  
CC cancer therapy. Vectors comprising the promoter and enhancer sequences

operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes, interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 568 BP; 142 A; 127 C; 143 G; 156 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTTATGTAGACACGCTTTCAAG 24  
|||  
203 CTTATGTAGACACGCTTTCAAG 180

RESULT 4  
ABX94595/c  
ID ABX94595 standard; DNA; 633 BP.  
AC ABX94595;  
XX  
XX 17-JUN-2003 (first entry)  
XX  
XX Human Mdr1 DNA SEQ ID 3.  
XX  
XX Mdr1; cytosine methylation; hydrogen sulphite; diagnose; dementia;  
XX 5-methylcytosine; amplification; prognosis; side effect; medication; bone;  
XX cancer; central nervous system disorder; aggression; muscle; endocrine;  
XX abnormal development; personality disorder; behavioural disorder; injury;  
XX brain damage; psychotic disorder; cardiovascular disease; infection;  
XX gastrointestinal tract; sexual malfunction; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO2003002760-A2.  
XX  
XX 09-JAN-2003.  
XX  
XX 27-JUN-2002; 2002MO-DE002433.  
XX  
XX 27-JUN-2001; 2001DE-01032212.  
XX  
XX (EPiG-) EPIGENOMICS AG.  
XX  
XX  
XX Dietler J, Leu E;  
XX  
XX WPI; 2003-201513/19.  
XX  
XX  
XX Determining cytosine methylation in a genomic DNA sample by treating with  
XX hydrogen sulfite and analyzing the result, to diagnose associated  
XX conditions including cancer and brain disorders.  
XX  
XX Example 1; Page 17; 38pp; German.  
XX  
XX This invention describes a novel method of determining cytosine  
XX methylation in a sample of genomic DNA which comprises treating the  
XX sample with hydrogen sulphite so that the cytosine is converted to uracil  
XX whilst 5-methylcytosine remains unchanged, amplifying sections of the DNA  
XX using at least 2 PCR primers and studying the base composition of both  
XX complementary amplified strands whereby methylation status is deduced  
XX from the difference in molecular weight of the two strands. The method is  
XX used to diagnose and/or prognosis unwanted side effects of medication,  
XX cancer, central nervous system disorders, aggression symptoms or  
XX behavioural disorders, clinical, psychological and social consequence of  
XX brain damage, psychotic and personality disorders, dementia and  
XX associated disorders, cardiovascular disease, malfunction, damage or  
XX disease of the gastrointestinal tract, breathing system, bone muscle,  
XX endocrine or metabolic system, injury, infection, abnormal development or  
XX sexual malfunction. This sequence represents the human Mdr1 DNA fragment  
XX amplified by the PCR primers represented in ABX94593 & ABX94594 and is  
XX used to illustrate the method of the invention

Sequence 633 BP; 161 A; 143 C; 165 G; 164 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 8; Length 633;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTTATGTAGACACGCTTTCAAG 24  
|||  
211 CTTATGTAGACACGCTTTCAAG 188

RESULT 5  
AAQ62614/c  
ID AAQ62614 standard; DNA; 1318 BP.  
AC AAQ62614;  
XX  
XX 25-MAR-2003 (revised)  
XX  
XX 17-JAN-1995 (first entry)  
XX  
XX Human mdr-1 promoter fragment.  
XX  
XX inducible promoter; cytostatic agent; adriamycin; vincristine;  
XX multiple drug resistance; mdr-1; mammalian expression vector;  
XX cancer therapy; ss.  
XX  
XX Homo sapiens.  
XX  
XX DE4238778-A1.  
XX  
XX 19-MAY-1994.  
XX  
XX 12-NOV-1992; 92DE-04238778.  
XX  
XX 12-NOV-1992; 92DE-04238778.  
XX  
XX 12-NOV-1992; 92DE-04238778.  
XX  
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
XX Stein U, Walthers W;  
XX  
XX WPI; 1994-168680/21.  
XX  
XX  
XX New mammalian expression vector useful for gene therapy, - comprising the  
XX promoter and/or the enhancer of the mdr-1 gene which is susceptible to  
XX cytostatic agents.  
XX  
XX Claim 2; Page 5; 7pp; German.  
XX  
XX This is a preferred fragment of the mdr-1 gene promoter, isolated from  
XX human DNA. The mdr-1 promoter and enhancer elements are inducible by  
XX cytostatic agents such as vincristine and adriamycin which are used in  
XX cancer therapy. Vectors comprising the promoter and enhancer sequences  
XX operably linked to heterologous genes coding for therapeutic agents are  
XX claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,  
XX interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the  
XX control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN  
XX field.)

Sequence 1318 BP; 430 A; 237 C; 277 G; 374 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 1318;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTTATGTAGACACGCTTTCAAG 24  
|||  
953 CTTATGTAGACACGCTTTCAAG 930

RESULT 6  
AAQ62613/c  
ID AAQ62613 standard; DNA; 1688 BP.

```

XX AC AA062613;
XX XX 25-MAR-2003 (revised)
DT 17-JAN-1995 (first entry)
XX XX Human mdr-1 promoter fragment.
DE XX
KW inducible promoter; cytosstatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; ss.
XX OS Homo sapiens.
XX PN DE4238778-A1.
XX PD 19-MAY-1994.
XX PF 12-NOV-1992; 92DE-04238778.
XX PR 12-NOV-1992; 92DE-04238778.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Stein U, Walther W;
XX DR WPI; 1994-168680/21.
XX XX New mammalian expression vector useful for gene therapy, - comprising the
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
PT cytosstatic agents.
XX PS Claim 2; Page 5; 7pp; German.
XX CC This is a preferred fragment of the mdr-1 gene promoter, isolated from
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
CC cytosstatic agents such as vincristine and adriamycin which are used in
CC cancer therapy. Vectors comprising the promoter and enhancer sequences
CC operably linked to heterologous genes coding for therapeutic agents are
CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 1688 BP; 556 A; 311 C; 371 G; 450 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 24; DB 2; Length 1688;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
DB 1323 CTTATGTAGACACGCTTTCAAG 1300

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XX PD 19-MAY-1994.
XX PF 12-NOV-1992; 92DE-04238778.
XX PR 12-NOV-1992; 92DE-04238778.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Stein U, Walther W;
XX DR WPI; 1994-168680/21.
XX XX New mammalian expression vector useful for gene therapy, - comprising the
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
PT cytosstatic agents.
XX PS Claim 2; Page 4; 7pp; German.
XX CC This is a preferred fragment of the mdr-1 gene promoter, isolated from
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
CC cytosstatic agents such as vincristine and adriamycin which are used in
CC cancer therapy. Vectors comprising the promoter and enhancer sequences
CC operably linked to heterologous genes coding for therapeutic agents are
CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 2090 BP; 714 A; 365 C; 444 G; 567 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 24; DB 2; Length 2090;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
DB 1725 CTTATGTAGACACGCTTTCAAG 1702

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RESULT 7
AA062612/c
ID AA062612 standard; DNA; 2090 BP.
XX AC AA062612;
XX XX
DT 25-MAR-2003 (revised)
DT 17-JAN-1995 (first entry)
XX XX Human mdr-1 promoter fragment.
DE XX
KW inducible promoter; cytosstatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; ss.
XX OS Homo sapiens.
XX PN DE4238778-A1.

```

```

RESULT 8
ABZ09897/c
ID ABZ09897 standard; DNA; 2932 BP.
XX AC ABZ09897;
XX XX
DT 16-JAN-2003 (first entry)
XX XX Human 5' and/or regulatory region of MDRI DNA SEQ ID NO:37.
DE XX
KW Human; haematopoietic cell proliferation disorder; cytosstatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX OS Homo sapiens.
XX PN WO20027272-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-EP003401.
XX PR 26-MAR-2001; 2001US-0278333P.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Berlin K, Braun A, Distler J, Gueclig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Lau B;
PI Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwabe I, Ziebarth H;
XX DR WPI; 2003-018942/01.

```

PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX  
 PS Claim 38; SEQ ID NO 37; 117pp; English.  
 XX  
 CC The present invention describes a method for detecting and  
 CC differentiating between hematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. AB209861 to AB21118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used for  
 CC differentiating between healthy hematopoietic cells and proliferative  
 CC disorder hematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of hematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of hematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC hematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of hematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 CC  
 XX Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;  
 S0  
 Query Match 100.0%; Score 24; DB 8; Length 2932;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTATGTAGACACGCTTTCAAG 24  
 DB 828 CTTATGTAGACACGCTTTCAAG 805  
 RESULT 9  
 ADB53945/c  
 ID ADB53945 standard; DNA; 2932 BP.  
 XX  
 AC ADB53945;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE MDRI genomic DNA region.  
 XX  
 KW colon cell proliferative disorder; non methylated CpG dinucleotide;  
 KW cytosinetic; cancer; adenoma; carcinoma; cytosine methylation state; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003072821-A2.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 27-FEB-2003; 2003WO-EP002035.  
 XX  
 PR 27-FEB-2002; 2002EP-00004551.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Lesche R;  
 XX  
 PI Rufen T, Schmitt A;  
 XX  
 DR WPI; 2003-731620/69.  
 XX  
 PT Detecting and differentiating between colon cell proliferative disorders  
 PT associated with a gene or its regulatory regions comprises contacting a  
 PT target nucleic acid in a biological sample obtained from the subject with

PT a reagent.  
 XX  
 PS Claim 46; SEQ ID NO 1; 74pp; English.  
 XX  
 CC The invention relates to a novel method for detecting and differentiating  
 CC between colon cell proliferative disorders associated with at least one  
 CC gene or its regulatory regions. The method comprises contacting a target  
 CC nucleic acid in a biological sample obtained from the subject with at  
 CC least one reagent or a series of reagents, where the reagent or series of  
 CC reagents, distinguishes between methylated and non methylated CpG  
 CC dinucleotides within the target nucleic acid. The molecules of the  
 CC invention demonstrate cytosinetic activity whilst the method may useful  
 CC for detecting and differentiating between colon cell proliferative  
 CC disorders, including cancers such as colon adenoma and colon carcinoma.  
 CC The PNA (peptide nucleic acid)-oligomers are useful as probes for  
 CC determining cytosine methylation state or single nucleotide  
 CC polymorphisms. The current sequence is that of the genomic DNA region of  
 CC the invention. This sequence is not shown within the specification but is  
 CC taken from Wipoweb.  
 XX  
 S0 Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 10; Length 2932;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTATGTAGACACGCTTTCAAG 24  
 DB 828 CTTATGTAGACACGCTTTCAAG 805  
 RESULT 10  
 ADE84005/c  
 ID ADE84005 standard; DNA; 2932 BP.  
 XX  
 AC ADE84005;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE 5' regulatory region of human gene MDRI.  
 XX  
 KW ds; lymphoid cell proliferative disorder; methylation;  
 KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;  
 KW diffuse large B-cell lymphoma; mantle cell lymphoma;  
 KW chronic lymphocytic leukemia; small lymphocytic lymphoma;  
 KW follicular lymphoma; diagnosis; prognosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003044226-A2.  
 XX  
 PD 30-MAY-2003.  
 XX  
 PF 25-NOV-2002; 2002WO-EP013265.  
 XX  
 PR 23-NOV-2001; 2001DE-01057491.  
 XX  
 PR 28-DEC-2001; 2001DE-01064501.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimrich I;  
 XX  
 DR WPI; 2003-457621/43.  
 XX  
 PT Detecting and differentiating between lymphoid cell proliferative  
 PT disorders comprises contacting a target nucleic acid with at least one  
 PT reagent that distinguishes between methylated and non-methylated CpG  
 PT dinucleotides.  
 XX  
 PS Disclosure; SEQ ID NO 1; 44pp; English.  
 XX  
 CC The invention relates to a method of detecting and differentiating  
 CC between lymphoid cell proliferative disorders associated with at least

CC one gene and/or their regulatory regions in a subject by contacting a  
 CC target nucleic acid in a biological sample obtained from the subject with  
 CC at least one reagent or series of reagents that distinguish between  
 CC methylated and non-methylated CpG dinucleotides within the target nucleic  
 CC acid. The genes and/or their regulatory regions are preferably selected  
 CC from MDR1, CSMK2B, EGR4, AR, BCL2, CDH1, CDKN1A, CDKN2A, CDKN2B, FOS,  
 CC MYC11, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN2A, CDKN2B, FOS,  
 CC GSTR1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TSGBR2, TP73, CDKN1C,  
 CC GSK3beta, ESRR1, APAF1, BAX1, BAX or HOKA5. Oligomers, peptide nucleic  
 CC acid (PNA)-oligonucleotides and/or isolated nucleic acids based on the sequences  
 CC of the genes are useful for detecting the methylation state of all the  
 CC CpG dinucleotides within one or more the sequences, or their complements,  
 CC for determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs), and for differentiating at least two of the medical  
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,  
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular  
 CC lymphoma. They are also useful for detecting of a predisposition to,  
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or  
 CC monitoring of lymphoid cell proliferative disorder. This sequence  
 CC represents the 5' and/or regulatory region from one of the above  
 CC mentioned genes.

CC Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 24; DB 10; Length 2932;  
 CC Best Local Similarity 100.0%; Pred. No. 0.15;  
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CTTATGTAGACACGCTTTCAAG 24  
 CC |||||  
 CC 828 CTTATGTAGACACGCTTTCAAG 805

CC RESULT 11

CC ADS88985/c  
 CC ID ADS88985 standard; DNA; 2932 BP.

CC ADS88985;

CC 18-NOV-2004 (first entry)

CC Human ABCB1 gene SEQ ID NO:1.

CC de; gene; human; cell proliferative disorder; breast; methylation;  
 CC cytochrome; gene therapy; single nucleotide polymorphism; SNP.

CC Homo sapiens.

CC WO2004035803-A2.

CC 29-APR-2004.

CC 01-OCT-2003; 2003WO-EP010881.

CC 01-OCT-2002; 2002DE-01045779.

CC 07-JAN-2003; 2003DE-01000096.

CC 17-APR-2003; 2003DE-01017955.

CC (EPIC-) EPIGENOMICS AG.

CC Fockens J, Harbeck N, Koenig T, Majer S, Martens J, Model F,  
 CC Nimnich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;  
 CC WPI; 2004-348468/32.

CC Predicting responsiveness of a subject with breast cell proliferative  
 CC disorder, useful for treating or differentiating breast cell  
 CC proliferative disorders comprises analyzing methylation pattern of a  
 CC genomic DNA from the subject.

CC Example 2; SEQ ID NO 1; 104pp; English.

CC The invention relates to a novel method for predicting the responsiveness

CC of a subject with a cell proliferative disorder of the breast tissues to  
 CC a therapy comprising analysing the methylation pattern of a target  
 CC nucleic acid by contacting at least one of the target nucleic acids in a  
 CC biological sample obtained from the subject prior to or during treatment.  
 CC The method of the invention has cytosine activity, and may have a use  
 CC in gene therapy. The set of oligonucleotides comprising at least two of  
 CC the oligomers are useful for detecting the cytosine methylation state  
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The  
 CC methods, nucleic acid, oligonucleotides, and kit are useful for the  
 CC treatment, characterization, classification and/or differentiation, of  
 CC breast cell proliferative disorder. The method is also useful for  
 CC predicting the responsiveness of a subject with a cell proliferative  
 CC disorder of the breast tissues to a therapy. The present sequence is used  
 CC in the exemplification of the invention.

CC Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 24; DB 13; Length 2932;  
 CC Best Local Similarity 100.0%; Pred. No. 0.15;  
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CTTATGTAGACACGCTTTCAAG 24  
 CC |||||  
 CC 828 CTTATGTAGACACGCTTTCAAG 805

CC RESULT 12

CC ABS98184/c  
 CC ID ABS98184 standard; DNA; 8573 BP.

CC ABS98184;

CC 23-DEC-2002 (first entry)

CC Human multidrug resistance gene promoter B and exons 1-3 sequence.

CC Human;

CC cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
 CC cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
 CC adrenergic receptor beta1; ADAR1; aryl hydrocarbon; AHR; MRP3; NR112;  
 CC aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
 CC cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 CC epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 CC glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
 CC HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
 CC NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase; SMO; SMT;  
 CC UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 CC UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;  
 CC multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 CC multidrug resistance associated protein 3; cancer; prostate;  
 CC acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 CC altered drug metabolism; cardiovascular function; colorectal tumour;  
 CC central nervous system; pulmonary; immunological; SNP;  
 CC single nucleotide polymorphism.

CC Homo sapiens.

CC WO200257410-A2.

CC 25-JUL-2002.

CC 28-NOV-2001; 2001WO-US044838.

CC 28-NOV-2000; 2000US-00724389.

CC (DNAS-) DNA SCI LAB INC.

CC Guida M, Hall J;  
 CC WPI; 2002-698522/75.

CC Isolated nucleic acid molecules having polymorphisms in known human genes  
 CC e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
 CC for locating, identifying and characterizing the genes responsible for



PT disorder-related traits.  
 XX  
 PS Example 22; Page 432-437; 714pp; English.  
 XX  
 CC This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
 CC cytochrome P450 02B1 (CYP45002B1), adrenoregic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
 CC transferase (HNMT), (Xelilkinin 2) KUK2, nicotinamide-N-methyl  
 CC sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), uridine kinase receptor (UPA), multidrug resistance  
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterizing the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502B1,  
 CC ARNT, EPHX2, GST12, HNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumors, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HNMT for altered berine  
 CC immunological or haematological function, in KUK2 for altered berine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC polymorphic DNA sequence of the invention  
 CC  
 XX  
 SQ Sequence 8573 BP; 2739 A; 1422 C; 1705 G; 2707 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 6; Length 8573;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTATGTAGACACGCTTTCAAG 24  
 DB 1773 CTTATGTAGACACGCTTTCAAG 1750  
 RESULT 13  
 AAD41243/C  
 ID AAD41243 standard; DNA; 10200 BP.  
 XX  
 AC AAD41243;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Human MDR1 gene 5' flanking region.  
 XX  
 KM Human, transgenic; reporter construct; CYP3A4; cytochrome P450;  
 KM transcriptional regulatory element; xenobiotic; steroid; MDR1;  
 KM p-glycoprotein; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200236784-A1.  
 XX PN  
 XX PD 10-MAY-2002.  
 XX

PF 01-NOV-2001; 2001WO-AU001407.  
 XX  
 PR 01-NOV-2000; 2000AU-00001161.  
 PR 10-MAY-2001; 2001AU-00004901.  
 XX  
 PA (UNSY) UNIV SYDNEY.  
 XX  
 PI Liddle C, Goodwin BJ, Robertson G;  
 XX  
 DR WPI; 2002-537301/57;  
 XX  
 PT Non-human mammal for determining the effect of a compound on regulation  
 PT of CYP3A4 gene expression, comprises a reporter construct for producing a  
 PT reporter linked to a transcriptional regulatory nucleic acid from a human  
 PT CYP3A4 gene.  
 XX  
 PS Claim 11; Page 83-92; 95pp; English.  
 XX  
 CC The invention relates to generation of non-human transgenic animals  
 CC comprising a reporter construct for producing a detectable amount of a  
 CC reporter molecule operably linked to a transcriptional regulatory nucleic  
 CC acid molecule from the human CYP3A4 gene. The invention also relates to  
 CC transgenic animal for analysing CYP3A4 cytochrome P450 gene regulation.  
 CC The non-human mammal of the invention is useful for determining whether a  
 CC compound is capable of affecting the transcription of a human CYP3A4  
 CC gene. It is also useful for determining the effect of a compound such as  
 CC a xenobiotic or steroid on the regulation of expression of the CYP3A4  
 CC gene in a human. The present sequence is 5' flanking region of human (p-  
 CC glycoprotein) MDR1 gene. This sequence is used as a regulatory element in  
 CC the invention  
 CC  
 XX  
 SQ Sequence 10200 BP; 3296 A; 1785 C; 1985 G; 3134 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 6; Length 10200;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTATGTAGACACGCTTTCAAG 24  
 DB 9051 CTTATGTAGACACGCTTTCAAG 9028  
 RESULT 14  
 ACF62751/C  
 ID ACF62751 standard; DNA; 177380 BP.  
 XX  
 AC ACF62751;  
 XX  
 DT 08-OCT-2003 (first entry)  
 XX  
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.  
 XX  
 KM Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;  
 KM cytochrome p450; subfamily 11A; nifedipine oxidase; polypeptide 5;  
 KM cytosstatic; gene; ds.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2003013534-A2.  
 XX PN  
 XX PD 20-FEB-2003.  
 XX  
 PF 23-JUL-2002; 2002WO-EP008219.  
 XX  
 PR 23-JUL-2001; 2001EP-00117608.  
 PR 24-MAY-2002; 2002EP-00011710.  
 XX  
 PA (EPID-) EPIDAUDROS BIOTECHNOLOGIE AG.  
 XX  
 XX Heinrich G, Kerb R;  
 XX PI  
 XX WPI; 2003-268144/26.  
 XX DR  
 XX

PT New use of irinotecan for preparation of compositions for treating cancer  
 PT in subject having genome with variant allele comprising cytochrome p450,  
 PT subfamily I1A, polypeptide 5 polynucleotide, termed CYP3A5.  
 PS  
 XX Disclosure; SEQ ID NO 683; 86pp; English.  
 CC The present invention describes the use of irinotecan (I) or its  
 CC derivative for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject having a genome with a variant  
 CC allele which comprises a cytochrome p450, subfamily I1A (nifedipine  
 CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have  
 CC cytostatic activity. The therapeutic applications of (I) is improved,  
 CC since it is possible to individually treat a subject with an appropriate  
 CC dosage and/or an appropriate derivative of (I). Therefore, an undesirable,  
 CC harmful or toxic effects are efficiently avoided. Unnecessary and  
 CC potentially harmful treatment of those subjects who do not respond to the  
 CC treatment with substances (nonresponders), as well as the development of  
 CC drug resistances due to suboptimal drug dosing can be avoided. ACP62200  
 CC to ACP62751 and ABM34912 to ABM35013 represent sequences used in the  
 CC exemplification of the present invention  
 CC  
 SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 8; Length 177380;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTATGTAGACAGCTTTCAAG 24  
 Db 140580 CTTATGTAGACAGCTTTCAAG 140557  
 RESULT 15  
 ID ADB20870/c  
 AC ADB20870;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DE MRP1 based cancer related nucleic acid SEQ ID NO:683.  
 XX  
 XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
 KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
 KM variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;  
 KM ds.  
 XX  
 OS Unidentified.  
 PN WO2003013533-A2.  
 XX  
 PD 20-FEB-2003.  
 PF 23-JUL-2002; 2002MO-EP008200.  
 PR 23-JUL-2001; 2001EP-00117608.  
 PR 24-MAY-2002; 2002EP-00011710.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Heinrich G, Kerb R;  
 XX  
 XX WPI; 2003-354397/33.  
 DR  
 XX  
 PT Use of irinotecan or its derivative for preparation of a pharmaceutical  
 PT composition for treating cancer in a subject having a genome with a  
 PT variant allele comprising a multidrug resistance protein 1  
 PT polynucleotide.  
 XX  
 PS Disclosure; SEQ ID NO 683; 100pp; English.  
 XX  
 CC The present invention describes a method for the use of irinotecan (I) or

CC its derivative for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject having a genome with a variant  
 CC allele which comprises a multidrug resistance protein 1 (MRP1)  
 CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative  
 CC can be used for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject, where the subject is a human  
 CC (preferably African or Asian) or a mouse. The present sequence represents  
 CC a sequence which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 8; Length 177380;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTATGTAGACAGCTTTCAAG 24  
 Db 140580 CTTATGTAGACAGCTTTCAAG 140557  
 Search completed: February 9, 2005, 16:05:52  
 Job time : 237.862 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 461.931 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-9

Perfect score: 24  
Sequence: 1 cttatgtacacgcgtcttcaag 24

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_pl:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_srs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	AX504306	AX504306 Sequence
2	24	100.0	24	AX504323	AX504323 Sequence
3	24	100.0	568	AR080195	AR080195 Sequence
4	24	100.0	633	AX701741	AX701741 Sequence
5	24	100.0	976	HUMMDR1A02	M29423 Human P-Gly
6	24	100.0	976	G19985	G19985 srsS10 Eric
7	24	100.0	1318	AR080194	AR080194 Sequence
8	24	100.0	1327	HUMMDR1P	L07624 Human multi
9	24	100.0	1688	AR080193	AR080193 Sequence
10	24	100.0	2090	AR080192	AR080192 Sequence
11	24	100.0	2117	A38669	A38669 Sequence 1
12	24	100.0	2186	HUMMDR1A	M57450 Human multi
13	24	100.0	2932	CQ806551	CQ806551 Sequence
14	24	100.0	2932	AX457064	AX457064 Sequence
15	24	100.0	2932	AX598697	AX598697 Sequence
16	24	100.0	2932	AX767353	AX767353 Sequence
17	24	100.0	2932	AX795658	AX795658 Sequence
18	24	100.0	2932	AX822109	AX822109 Sequence
19	24	100.0	2932	AX825749	AX825749 Sequence

c	20	24	100.0	2932	9	HSMDR1A
c	21	24	100.0	177380	6	AX706985
c	22	24	100.0	177380	6	AX707915
c	23	24	100.0	177380	9	AC002457
c	24	23	95.8	23	6	AX504348
c	25	23	95.8	23	6	AX504352
c	26	22	91.7	22	6	AX504349
c	27	22	91.7	22	6	AX504353
c	28	21	87.5	21	6	AX504350
c	29	21	87.5	21	6	AX504351
c	30	21	87.5	21	6	AX504354
c	31	20.8	86.7	110000	2	AC110967-2
c	32	20.4	85.0	158344	2	CR352257
c	33	20	83.3	20	6	AX504355
c	34	19.8	82.5	633	6	AX701744
c	35	19.8	82.5	2010	6	AX457065
c	36	19.8	82.5	2932	6	CQ806797
c	37	19.8	82.5	2932	6	AX529569
c	38	19.8	82.5	2932	6	AX598827
c	39	19.8	82.5	2932	6	AX767413
c	40	19.8	82.5	2932	6	AX795733
c	41	19.8	82.5	2932	6	AX822241
c	42	19.8	82.5	2932	6	AX825881
c	43	19.8	82.5	110000	2	AC130739-1
c	44	19.8	82.5	164545	2	CR354542
c	45	19.8	82.5	174986	5	AL935126

#### ALIGNMENTS

RESULT 1	AX504306	AX504306	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504306	Sequence 9 from Patent WO0234291.				
DEFINITION	AX504306	AX504306				
ACCESSION	AX504306.1	GI:23386124				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM		Homo sapiens (human)				
REFERENCE		Colgan, S.P.				
AUTHORS		Compositions and methods for treating hematologic malignancies and				
TITLE		multiple drug resistance				
JOURNAL		Patent: WO 0234291-A 9 02-MAY-2002;				
FEATURES		THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)				
source		location/Qualifiers				
ORIGIN		1..24				
Query Match		/organism="Homo sapiens"				
Best Local Similarity		/mol_type="unassigned DNA"				
Matches		/db_xref="taxon:9606"				
24; Conservative						
0; Mismatches						
0; Indels						
0; Gaps						
0;						
RESULT 2	AX504323/c	AX504323	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	Sequence 26 from Patent WO0234291.				
DEFINITION	AX504323	AX504323				
ACCESSION	AX504323.1	GI:23386135				
VERSION						
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Colgan, S.P.  
TITLE Compositions and methods for treating hematologic malignancies and multiple drug resistance  
JOURNAL Patent: WO 0234291-A 26 02-MAY-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)  
FEATURES  
source 1.24  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24  
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24 CTTATGTAGACACGCTTTCAAG 1

Db 24 CTTATGTAGACACGCTTTCAAG 1

RESULT 3  
AR080195/c 568 bp DNA linear PAT 31-AUG-2000  
LOCUS AR080195  
DEFINITION Sequence 4 from patent US 5968735.  
ACCESSION AR080195  
VERSION AR080195.1 GI:10006930  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 568)  
AUTHORS Stein, U. and Walther, W.  
TITLE Vector for the expression of therapy-relevant genes  
JOURNAL Patent: US 5968735-A 4 19-OCT-1999;  
FEATURES  
source 1.568  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 568;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24  
|||||  
203 CTTATGTAGACACGCTTTCAAG 180

Db 203 CTTATGTAGACACGCTTTCAAG 180

RESULT 4  
AX701741/c 633 bp DNA linear PAT 03-APR-2003  
LOCUS AX701741  
DEFINITION Sequence 3 from Patent W003002760.  
ACCESSION AX701741  
VERSION AX701741.1 GI:29537273  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.  
AUTHORS Distler, J. and Leu, E.  
TITLE Method for detecting cytosine methylation by comparatively analysing single strands of amplification  
JOURNAL Patent: WO 03002760-A 3 09-JAN-2003;  
FEATURES  
source 1.633  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 633;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24  
|||||  
211 CTTATGTAGACACGCTTTCAAG 188

Db 211 CTTATGTAGACACGCTTTCAAG 188

RESULT 5  
HUMMDR1A02/c 976 bp DNA linear PRI 08-JAN-1995  
LOCUS HUMMDR1A02  
DEFINITION Human P-glycoprotein (MDR1) gene, 5' flank.  
ACCESSION M29423 J05168 M18754  
VERSION M29423.1 GI:187472  
KEYWORDS P-glycoprotein; multidrug resistance.  
SEGMENT 2 of 26  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 976)  
AUTHORS Veda, K., Pastan, I., and Gottesman, M.M.  
TITLE Isolation and sequence of the promoter region of the human multidrug-resistance (P-glycoprotein) gene  
JOURNAL J. Biol. Chem. 262 (36), 17432-17436 (1987)  
MEDLINE 88087023  
PUBMED 2891692  
REFERENCE 2 (bases 1 to 976)  
AUTHORS Chen, C.-J., Clark, D., Veda, K., Pastan, I., Gottesman, M.M. and Roninson, I.B.  
TITLE Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoproteins  
JOURNAL J. Biol. Chem. 265 (1), 506-514 (1990)  
MEDLINE 1967175  
PUBMED  
COMMENT Original source text: Human multidrug resistant cell line KB-V1 DNA.  
[2] reviews (1).  
Draft entry and computer-readable sequence for [1] kindly submitted by I.B. Roninson, 27-OCT-1989.  
FEATURES  
source 1.976  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/map="7g21"  
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/gene="PGY1"  
/note="PGY1 mRNA and intron (alt.); G00-120-712"  
intron <1..244  
/gene="PGY1"  
/note="PGY1, intron A"  
prim\_transcript 435..>976  
/gene="PGY1"  
/note="PGY1 mRNA and intron (alt.)"  
intron 569..>976  
/gene="PGY1"  
/note="PGY1, intron A"

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 976;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24  
|||||  
189 CTTATGTAGACACGCTTTCAAG 166

Db 189 CTTATGTAGACACGCTTTCAAG 166

**RESULT 6**  
**LOCUS** G19985 976 bp DNA linear STS 28-SEP-1998  
**DEFINITION** SMS10 Eric D. Green Homo sapiens STS genomic, sequence tagged site  
**ACCESSION** G19985  
**VERSION** G19985.1 GI:1254684  
**KEYWORDS** STS.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 976)  
**AUTHORS** Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F., Weintrub, L.A., Mohr-Tidwell, R.M., Peluso, D.C., Fulton, R.S., Leckie, M.P. and Green, E.D.  
**TITLE** A collection of 1814 human chromosome 7-specific STS  
**JOURNAL** Genome Res. 7 (1), 59-64 (1997)  
**MEDLINE** 9037602  
**PUBMED** 9037602  
**REFERENCE** 2 (bases 1 to 976)  
**AUTHORS** Green, E.D.  
**TITLE** Human chromosome 7 STS (1997)  
**JOURNAL** Unpublished (1997)  
**COMMENT** Synonyms: PGY1  
**DB** GDB: GDB:583426  
**GENE** GDB: DSEG: PGY1  
**CONTACT** Eric D. Green  
**Genome Technology Branch**  
**National Human Genome Research Institute/NIH**  
**49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892**  
**Tel: 3014020201**  
**Fax: 3014024735**  
**Email: egreen@hgrl.nih.gov**  
**Primer A: ACCGAGCCGACATCTCC**  
**Primer B: AGCTTCCTGTGGCAAGAG**  
**STS size: 180**  
**PCR Profile:**  
**Presoak:** 0 degrees C for 0.00 minute(s)  
**Denaturation:** 92 degrees C for 1.00 minute(s)  
**Annealing:** 68 degrees C for 2.00 minute(s)  
**Polymerization:** 72 degrees C for 2.00 minute(s)  
**PCR Cycles:** 35  
**Thermal Cycler:** PerkinElmer TC  
**Protocol:**  
**Template:** 30-100 ng  
**Primer:** each 1 uM  
**dNTPs:** each 200 uM  
**Taq Polymerase:** 0.05 units/uL  
**Total Vol:** 5 uL  
**Buffer:**  
**MgCl2:** 1.5 mM  
**KCl:** 50 mM  
**Tris-HCl:** 10 mM  
**pH:** 8.3  
**FEATURES**  
**source** 1..976  
**Location/Qualifiers**  
**1..976**  
**/organism="Homo sapiens"**  
**/mol\_type="genomic DNA"**  
**/db\_xref="taxon:9606"**  
**/map="7"**  
**/clone\_lib="Eric D. Green"**  
**1..976**  
**/gene="PGY1"**  
**253..432**

**Query Match** 100.0%; Score 24; DB 11; Length 976;  
**Best Local Similarity** 100.0%; Pred. No. 1.1;  
**Matches** 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**ORIGIN** primer\_bind complement (413..432)  
**Qy** 1 CTTATGTAGACGCTCTTCAAAG 24  
**Db** 189 CTTATGTAGACGCTCTTCAAAG 166  
**RESULT 7**  
**LOCUS** AR080194 1318 bp DNA linear PAT 31-AUG-2000  
**DEFINITION** Sequence 3 from patent US 5968735.  
**ACCESSION** AR080194  
**VERSION** AR080194.1 GI:10006929  
**KEYWORDS** .  
**SOURCE** Unknown.  
**ORGANISM** Unknown.  
**REFERENCE** 1 (bases 1 to 1318)  
**AUTHORS** Stein, U. and Walther, W.  
**TITLE** Vector for the expression of therapy-relevant genes  
**JOURNAL** Patent: US 5968735-A 3 19-OCT-1999;  
**FEATURES** Location/Qualifiers  
**source** 1..1318  
**/organism="Unknown"**  
**/mol\_type="unassigned DNA"**  
**ORIGIN**  
**Query Match** 100.0%; Score 24; DB 6; Length 1318;  
**Best Local Similarity** 100.0%; Pred. No. 1;  
**Matches** 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**Qy** 1 CTTATGTAGACGCTCTTCAAAG 24  
**Db** 953 CTTATGTAGACGCTCTTCAAAG 930  
**RESULT 8**  
**LOCUS** HUMMDR1P/C 1327 bp DNA linear PRI 09-JAN-1995  
**DEFINITION** Human multidrug resistant P glycoprotein (MDR1, PGY1) gene, 5' flank.  
**ACCESSION** L07624  
**VERSION** L07624.1 GI:187500  
**KEYWORDS** MDR1 gene; P-glycoprotein; multidrug resistance protein.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.**  
**REFERENCE** 1 (bases 1 to 1327)  
**AUTHORS** Madden, M.J., Morrow, C.S., Nakagawa, M., Goldsmith, M.E., Fairchild, C.R. and Cowan, K.H.  
**TITLE** Identification of 5' and 3' sequences involved in the regulation of transcription of the human mdr1 gene in vivo  
**JOURNAL** U. Biol. Chem. 268 (11), 8290-8297 (1993)  
**MEDLINE** 93216814  
**PUBMED** 8096520  
**COMMENT** Original source text: Homo sapiens (tissue library: lambda Charon 4a) bone marrow DNA.  
**FEATURES** Location/Qualifiers  
**source** 1..1327  
**/organism="Homo sapiens"**  
**/mol\_type="genomic DNA"**  
**/db\_xref="taxon:9606"**  
**/map="7q21"**  
**/cell\_type="Leukocyte"**

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Query Match	Best Local Match	Similarity	Score	DB	Length
Query Match	Best Local Match	Similarity	Score	DB	Length
Matches	Matches	24; Conservative	0; Mismatches	0; Indels	0; Gaps
1	1	CTTATGTAGACACGCTTTTCAAG	24		
Db	1323	CTTATGTAGACACGCTTTTCAAG	1300		
RESULT 10	AR080192/c	2090 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR080192	Sequence 1 from patent US 5968735.			
DEFINITION	AR080192	AR080192.1 GI:10006927			
ACCESSION	AR080192.1	GI:10006927			
VERSION	Unknown.	Unknown.			
KEYWORDS	Unclassified.	Unclassified.			
ORGANISM	1 (bases 1 to 2090)	Stein, U. and Walther, W.			
REFERENCE	Vector for the expression of therapy-relevant genes	Patent: US 5968735-A 1 19-Oct-1999;			
AUTHORS	location/Qualifiers	1. .2090			
TITLE	source	/organism="unknown"			
JOURNAL		/mol_type="unassigned DNA"			
FEATURES					
ORIGIN					
Query Match	Best Local Match	Similarity	Score	DB	Length
Matches	Matches	24; Conservative	0; Mismatches	0; Indels	0; Gaps
1	1	CTTATGTAGACACGCTTTTCAAG	24		
Db	1725	CTTATGTAGACACGCTTTTCAAG	1702		
RESULT 11	A38669/c	2117 bp	DNA	linear	PAT 11-NOV-1999
LOCUS	A38669	Sequence 1 from Patent WO9411522.			
DEFINITION	A38669	A38669.1 GI:2295152			
ACCESSION	A38669.1	GI:2295152			
VERSION	Unknown.	Unknown.			
KEYWORDS	Homo sapiens (human)	Homo sapiens			
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 2117)	Stein, U. and Walther, W.			
AUTHORS	VECTOR FOR THE EXPRESSION OF THERAPY-RELEVANT GENES	Patent: WO 9411522-A 1 26-MAY-1994;			
TITLE	MAX DELBRUECK CT FUER MOLEKULA (DE)	Other publication DE 4238778 940519.			
JOURNAL	location/Qualifiers	1. .2117			
COMMENT		/organism="Homo sapiens"			
FEATURES		/mol_type="unassigned DNA"			
SOURCE		/db_xref="taxon:9606"			
		/clone="CVS-SM1"			
		/cell_type="SARCOMAS"			
		/tissue_type="TUMORS"			
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ORIGIN					
Query Match	Best Local Match	Similarity	Score	DB	Length
Matches	Matches	24; Conservative	0; Mismatches	0; Indels	0; Gaps
1	1	CTTATGTAGACACGCTTTTCAAG	24		
Db	1323	CTTATGTAGACACGCTTTTCAAG	1300		
RESULT 10	AR080192/c	2090 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR080192	Sequence 1 from patent US 5968735.			
DEFINITION	AR080192	AR080192.1 GI:10006927			
ACCESSION	AR080192.1	GI:10006927			
VERSION	Unknown.	Unknown.			
KEYWORDS	Unclassified.	Unclassified.			
ORGANISM	1 (bases 1 to 2090)	Stein, U. and Walther, W.			
REFERENCE	Vector for the expression of therapy-relevant genes	Patent: US 5968735-A 1 19-Oct-1999;			
AUTHORS	location/Qualifiers	1. .2090			
TITLE	source	/organism="unknown"			
JOURNAL		/mol_type="unassigned DNA"			
FEATURES					
ORIGIN					
Query Match	Best Local Match	Similarity	Score	DB	Length
Matches	Matches	24; Conservative	0; Mismatches	0; Indels	0; Gaps
1	1	CTTATGTAGACACGCTTTTCAAG	24		
Db	1725	CTTATGTAGACACGCTTTTCAAG	1702		
RESULT 11	A38669/c	2117 bp	DNA	linear	PAT 11-NOV-1999
LOCUS	A38669	Sequence 1 from Patent WO9411522.			
DEFINITION	A38669	A38669.1 GI:2295152			
ACCESSION	A38669.1	GI:2295152			
VERSION	Unknown.	Unknown.			
KEYWORDS	Homo sapiens (human)	Homo sapiens			
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases				

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 DB 1725 CTTATGTAGACACGCTTTTCAAG 1702

RESULT 12  
 HUMMDRIA 2186 bp DNA linear PRI 07-JAN-1995  
 LOCUS Human multidrug-resistance (MDR1) gene, exon 1.  
 DEFINITION M57450 J05673  
 ACCESSION M57450.1 GI:187470  
 VERSION multidrug resistance.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Kohno,K., Sato,S., Uchiumi,T., Takano,H., Kato,S. and Kuwano,M.  
 TITLE Tissue-specific enhancer of the human multidrug-resistance (MDR1) gene

JOURNAL J. Biol. Chem. 265 (32), 19690-19696 (1990)

MEDLINE 91060578

COMMENT Original source text: Human cancer multidrug-resistant cell line KB-C1 DNA.

FEATURES  
 source location/Qualifiers  
 1..2186 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
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 /cell\_line="KB-C1"  
 /tissue\_type="KB cancer"  
 623..627 /standard\_name="5' insertion target sequence"  
 628..950 /title="Alu repeat"  
 /rpt\_family="Alu repeat"  
 951..955 /standard\_name="3' insertion target sequence"  
 2029..2186 /gene="PGY1"  
 2029..2158 /gene="PGY1"  
 /product="multidrug resistance protein"  
 /note="G00-120-712"  
 2159..2186 /gene="PGY1"  
 /note="G00-120-712"  
 /number=1

# ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 2186;  
 Best Local Similarity 100.0%; Pred. No. 0.95;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 DB 1780 CTTATGTAGACACGCTTTTCAAG 1757

RESULT 13  
 CQ806551 2932 bp DNA linear PAT 10-MAY-2004  
 LOCUS CQ806551/C  
 DEFINITION Sequence 1 from Patent WO2004035803.  
 ACCESSION CQ806551  
 VERSION CQ806551.1 GI:47111933  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Fockens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,

Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.  
 TITLE Method and nucleic acids for the improved treatment of breast cell  
 JOURNAL proliferative disorders  
 Patent: WO 2004035803-A 1 29-APR-2004;  
 Epigenomics AG (DE)

FEATURES  
 source location/Qualifiers  
 1..2932 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
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Query Match 100.0%; Score 24; DB 6; Length 2932;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 DB 828 CTTATGTAGACACGCTTTTCAAG 805

RESULT 14  
 AX457064 2932 bp DNA linear PAT 06-JUL-2002  
 LOCUS AX457064  
 DEFINITION Sequence 25 from Patent WO231186.  
 ACCESSION AX457064  
 VERSION AX457064.1 GI:21715846  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Berlin,K.  
 TITLE Method for the detection of cytosine methylations  
 JOURNAL Patent: WO 0231186-A 25 18-APR-2002;  
 Epigenomics AG (DE)

FEATURES  
 source location/Qualifiers  
 1..2932 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
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 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 DB 828 CTTATGTAGACACGCTTTTCAAG 805

RESULT 15  
 AX598697 2932 bp DNA linear PAT 14-FEB-2003  
 LOCUS AX598697/C  
 DEFINITION Sequence 37 from Patent WO02077272.  
 ACCESSION AX598697  
 VERSION AX598697.1 GI:28398833  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,  
 Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Ley,E.,  
 Lewin,A., Lipicher,E., Maier,S., Model,F., Mueller,V., Otto,T.,  
 Pelet,C. and Ziebarth,H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell  
 JOURNAL proliferative disorders  
 Patent: WO 02077272-A 37 03-OCT-2002;

Epigenomics AG (DE)  
 FEATURES  
 Location/Qualifiers  
 source 1..2932  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Query Match 100.0%; Score 24; DB 6; Length 2932;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||  
 Db 828 CTTATGTAGACGCTTTCAAG 805

Search completed: February 9, 2005, 17:01:53  
 Job time : 464.931 secs



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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2350.9 Seconds  
(without alignments)  
388.593 Million cell updates/sec

Title: US-10-007-255-9  
Perfect score: 24  
Sequence: 1 ctatctgagacacgtcttccaag 24

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gse1: \*  
9: gb\_gse2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	85.0	213	7	CN813365 Fg06_06h1
2	19.8	82.5	671	2	BB662530 BB662530
3	19.2	80.0	780	8	B2984511 PUGIE79TD
4	19.2	80.0	780	8	CC65078 PUMME62TB
5	19.2	80.0	816	9	BZ984507 PUGIE79TB
6	19.2	80.0	889	8	CG457221 PUIK34TD
7	18.8	78.3	426	6	CD476851 eca01-18m
8	18.8	78.3	627	9	BH332334 CH230-125
9	18.8	78.3	632	9	CL706910 OR_BBA002
10	18.8	78.3	731	9	CL70267 OR_BBA004
11	18.8	78.3	765	9	CL807004 OR_Cha002
12	18.8	76.7	526	1	AI332619 qg28a04.x
13	18.4	75.8	180	8	BH812962 SALK_0635
14	18.2	75.8	197	8	BZ290962 SALK_1122
15	18.2	75.8	241	2	AM999627 MR0-BN007
16	18.2	75.8	323	1	TS3393 yb47c09.r1
17	18.2	75.8	433	7	AV790780 AV790780
18	18.2	75.8	433	7	N96634 21309 lambda
19	18.2	75.8	433	7	CC053247 SALK_0412
20	18.2	75.8	513	4	BI813622 L002D03.O
21	18.2	75.8	513	4	CV070774 CS_g11_30
22	18.2	75.8	539	7	AV558834 AV558834
23	18.2	75.8	575	1	CV071055 CS_g11_39
24	18.2	75.8	596	7	CV071055 CS_g11_39

C 25	18.2	75.8	652	8	BZ845681	BZ845681 CH240_291
C 26	18.2	75.8	672	1	A1729367	A1729367 BNLG1131
C 27	18.2	75.8	685	1	AG044289	AG044289 Pan troy1
C 28	18.2	75.8	686	4	BG440031	BG440031 GA_EA000
C 29	18.2	75.8	691	2	BB045461	BB045461 BB045461
C 30	18.2	75.8	720	6	CB665945	CB665945 OSJNE02A
C 31	18.2	75.8	737	6	CB665934	CB665934 OSJNE02B
C 32	18.2	75.8	749	4	BI737199	BI737199 60358225
C 33	18.2	75.8	768	3	CNS0A6C1	BX825649 Arabidops
C 34	18.2	75.8	811	9	CNS06DK0	AL393936 T7 end of
C 35	18.2	75.8	975	9	CR012766	CR012766 Forward B
C 36	18.2	75.8	986	9	CR248215	CR248215 Forward B
C 37	18.2	75.8	1474	6	CA156945	CA156945 SCEOR2302
C 38	18.2	75.8	512	8	AQ020267	AQ020267 CIT-HSP-2
C 39	18.2	75.8	569	8	BZ603334	BZ603334 WHAC067TF
C 40	17.8	74.2	516	7	CK507205	CK507205 rswcc0_01
C 41	17.8	74.2	542	2	BF195858	BF195858 7086B09.x
C 42	17.8	74.2	542	2	BF197586	BF197586 7085B09.x
C 43	17.8	74.2	555	8	AZ009974	AZ009974 RPCI-23-2
C 44	17.8	74.2	559	9	CR343395	CR343395 Medicago
C 45	17.8	74.2	585	9	CL376034	CL376034 RPCI44_44

ALIGNMENTS

RESULT 1  
CN813365/c 213 bp mRNA linear EST 01-JUN-2004  
LOCUS Fg06\_06h10\_R Fg06\_AAFc\_ECOrc Fusarium graminearum perithecia  
DEFINITION Gibberella zeae cDNA clone Fg06\_06h10, mRNA sequence.  
VERSION CN813365  
KEYWORDS CN813365.1 GI:47837376  
SOURCE EST.  
ORGANISM Gibberella zeae (anamorph: Fusarium graminearum)  
Gibberella zeae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE  
AUTHORS Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J.,  
Coutoux,P., De Moore,A., Hattori,J.T., Lacroix,C., Masotti,M.,  
Robert,L.S., Singh,J.A., Spriett,D. and Tinker,N.A.  
Expressed Sequence Tags from Fusarium graminearum enriched for late  
stage perithecia  
Unpublished (2004)  
JOURNAL  
COMMENT Contact: Harris, Linda J.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,  
CANADA  
Tel: (613) 759-1314  
Fax: (613) 759-6566  
Email: harris@agr.gc.ca.

FEATURES  
source location/Qualifiers  
1..213  
/organism="Gibberella zeae"  
/mol\_type="mRNA"  
/strain="DAOM 180378"  
/db\_xref="taxon:5518"  
/clone="Fg06\_06h10"  
/dev\_stage="Sexual"  
/lab\_host="F. coli DH10B"  
/clone\_lib="Fg06\_AAFc\_ECOrc\_Fusarium graminearum perithecia"

ORIGIN  
/note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown on carrot agar at 20C until confluent; perithecia induced with Tween 40 solution (2% v/v). Fruiting bodies were collected 20 days after induction. Total RNA was extracted using Trizol. cDNAs were amplified using Invitrogen Generacer kit. cDNA was not fractionated and was bidirectionally cloned."

Query Match 85.0%; Score 20.4; DB 7; Length 213;  
 Best Local Similarity 95.5%; Pred. No. 50;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TATGTAGACAGCTCTTCAAG 24  
 |||||  
 186 TATGTAGACAGCTTCAAG 165

## RESULT 2

BB662530/c

LOCUS BB662530 RIKEN full-length enriched, 15 days embryo head Mus 671 bp mRNA linear EST 26-OCT-2001  
 DEFINITION Musculus cDNA clone D93005N11 5', mRNA sequence.

ACCESSION

BB662530

VERSION

BB662530.1

KEYWORDS

GI:16496284

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 671)

AUTHORS

Arikawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
 Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
 Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

TITLE

Unpublished (2001)

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Saito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE

10 (10), 1617-1630 (2000)

AUTHORS

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,  
 Sugahara, Y. and Hayashizaki, Y.

JOURNAL

COMMENT

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

REFERENCE

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I.,  
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
 Hayashizaki, Y.

TITLE

Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

JOURNAL

COMMENT

Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.

FEATURES

source

Location/Qualifiers

1..671

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="D93005N11"

/sex="mixed"

/tissue\_type="head"

ORIGIN

Query Match 80.0%; Score 19.2; DB 8; Length 780;  
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;

Matches

21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TATGTAGACAGCTCTTCAAG 24  
 |||||  
 472 TATGTAGACAGCTTCAAG 450

RESULT 3

BZ984511

LOCUS BZ984511 780 bp DNA linear GSS 25-MAR-2003  
 DEFINITION PUGIE797D ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTa390M13,  
 genomic survey sequence.

ACCESSION

BZ984511

VERSION

BZ984511.1

KEYWORDS

GI:29219382

SOURCE

GSS.

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 780)  
 Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
 Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
 Bennettzen, J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other GSSs: PUGIE797B  
 Contact: Cathy Whitehead  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitehead@tigr.org  
 Seq primer: TP  
 Class: shared ends.

FEATURES

source

Location/Qualifiers

1..780

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBTa390M13"

/clone\_id="ZM.0.6.1.0 KB"

/note="Vector: PCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN

Query Match 80.0%; Score 19.2; DB 8; Length 780;  
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 380 CTTATGTAGACATGCTTTTCAAG 403

RESULT 4  
 CC365078 780 bp DNA linear GSS 16-MAY-2003  
 LOCUS PUBM622TB ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMMBTa483K03,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC365078  
 VERSION CC365078.1 GI:30834478  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 780)  
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other GSSs: PUBM622D  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..780  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_id="ZMMBTa483K03"  
 /clone\_1lb="ZM\_0.6\_1.0\_KB"  
 /note="vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 cot selected genomic DNA library"

ORIGIN  
 Query Match 80.0%; Score 19.2; DB 8; Length 780;  
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 103 CTTATGTAGACATGCTTTTCAAG 80

RESULT 5  
 BZ984507 816 bp DNA linear GSS 25-MAR-2003  
 LOCUS PUBI879TB ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMMBTa390M13,  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ984507  
 VERSION BZ984507.1 GI:29219374  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 816)  
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.

TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Other\_GSSs: PUBI879TB  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..816  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_id="ZMMBTa390M13"  
 /clone\_1lb="ZM\_0.6\_1.0\_KB"  
 /note="vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 cot selected genomic DNA library"

ORIGIN  
 Query Match 80.0%; Score 19.2; DB 8; Length 816;  
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24  
 |||||  
 620 CTTATGTAGACATGCTTTTCAAG 597

RESULT 6  
 CG457221 889 bp DNA linear GSS 17-SEP-2003  
 LOCUS PUIK34TDB ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMMBTa0602F19,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG457221  
 VERSION CG457221.1 GI:34842221  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 889)  
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other\_GSSs: PUIK34TDB  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..889  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_id="ZMMBTa0602F19"  
 /clone\_1lb="ZM\_0.6\_1.0\_KB"  
 /note="vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 cot selected genomic DNA library"

ORIGIN  
 Query Match 80.0%; Score 19.2; DB 9; Length 889;

Best Local Similarity 87.5%; Pred. No. 2.3e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTTATGTAGACACGCTTTCAAG 24  
|||||  
550 CTTATGTAGACACGCTTTCAAG 573

RESULT 7  
CL745575

LOCUS CL745575 426 bp DNA linear GSS 27-JUL-2004  
DEFINITION OR\_BB0082M07.r OR\_BBA Oryza rufipogon genomic clone OR\_BB0082M07

ACCESSION CL745575  
VERSION CL745575.1 GI:50686923

KEYWORDS GSS

SOURCE Oryza rufipogon

ORGANISM Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 426)

AUTHORS Kim,H., Yu,Y., Stum,D., Yeat,D., Rao,K., Luo,M., Jettly,R.,  
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMAP Project

JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595  
Fax: 520 621 1259

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: TCA TCA TTA GGC ACC CCA

Insert Length: 161 Std Error: 0.00  
Plate: 0082 row: M column: 07

Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source Location/Qualifiers

1..426  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"

/db\_xref="taxon:4529"  
/clone="OR\_BB0082M07"

/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"

/clone\_lib="OR\_BBA"  
/note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN

Query Match 78.3%; Score 18.8; DB 9; Length 426;  
Best Local Similarity 90.9%; Pred. No. 3.3e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TATGTAGACACGCTTTCAAG 24  
|||||  
151 TATGTAGACACGCTTTCAAG 172

Db 151 TATGTAGACACGCTTTCAAG 172

RESULT 8  
CD476851 464 bp mRNA linear EST 04-JUN-2003  
LOCUS eca01-18ms1-f06 Eca01 Eschscholzia californica cDNA clone  
DEFINITION eca01-18ms1-f06 5', mRNA sequence.

ACCESSION CD476851  
VERSION CD476851  
KEYWORDS EST

SOURCE CD476851.1 GI:31398119

ORGANISM Eschscholzia californica (California poppy)  
Eschscholzia californica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;

REFERENCE 1 (bases 1 to 464)

AUTHORS Papaveraceae; Eschscholziaceae; Eschscholzia.  
dePamphilis,C., Carlson,J., Ma,H., Tanksley,S., Field,D.,  
Leebens-Mack,J., Arrington,J., Zahn,L.M., Kong,H., Ilu,D.,  
Druckemiller,M., Landherr,L., Hu,Y., Plock,S., Wall,K.,  
Chioean,S., Albert,Y., Doyle,J., Frohlich,M., Miller,M.,  
Oppenheimer,D., Solis,D., Solis,P. and Theissen,G.

Generation of ESTs from early flower buds of Eschscholzia  
californica

Unpublished (2002)

CONTACT: Claude dePamphilis or James Leebens-Mack  
Mueller Laboratory  
Penn State University

208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
State University, University Park, PA 16802, USA

Tel: 814 863 6413  
Fax: 814 865 9131

Email: [cwd3@psu.edu](mailto:cwd3@psu.edu) or [jhl10@psu.edu](mailto:jhl10@psu.edu)

The sequence provided is trimmed of vector and low quality regions.  
Full sequence and original trace file are available from the Plant  
Genome Network website (<http://pgn.cornell.edu>)

Plate: eca01-18ms1 row: f column: 06  
Seq primer: M13F.

FEATURES  
source Location/Qualifiers

1..464  
/organism="Eschscholzia californica"  
/mol\_type="mRNA"

/cultivar="Aurantia Orange"  
/db\_xref="taxon:3467"

/clone="eca01-18ms1-f06"  
/issue\_type="flower buds <= 2.5mm"

/dev\_stage="millimeter buds"  
/lab\_host="SOLR"

/clone\_lib="eca01"

/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;  
Site 2: XhoI; plants were grown in greenhouse at Penn  
State from commercially available seeds. Only floral buds  
with diameter of 2.5 mm or less were collected. This is a  
directionally cloned, non-normalized library. Avg. insert  
length: 1702; Primers: M13F and M13R; Antibiotic: 50 ug/ml  
Ampicillin; Primary filter: 766 pin total; Amplified filter:  
1.68E11 pin/ml; Mass Excised filter: 5.6E8 total; This  
library has been generated by the Floral Genome Project  
(FGP). We would like to thank Huck Life Sciences  
Consortium for their assistance. The Floral Genome Project  
is funded by NSF's Plant Genome Research Program  
(DBI-0115684). More information about the project can be  
obtained at <http://fgp.bio.psu.edu>"

ORIGIN

Query Match 78.3%; Score 18.8; DB 6; Length 464;  
Best Local Similarity 90.9%; Pred. No. 3.3e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TATGTAGACACGCTTTCAAG 24  
|||||  
332 TATGTAGACACGCTTTCAAG 311

Db 332 TATGTAGACACGCTTTCAAG 311

RESULT 9  
BH332334 627 bp DNA linear GSS 03-DEC-2001  
LOCUS CH230-125M16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
DEFINITION CH230-125M16, genomic survey sequence.

ACCESSION BH332334  
VERSION BH332334  
KEYWORDS GSS

SOURCE BH332334.1 GI:17263048

ORGANISM Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 627)

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K., Shvartsbeyn, A., Gebregorjls, B., Ovetton, L., Russell, D., Chen, D., R. 1998, F., de Jong, P., and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
Other GSSs: CH230-125M16.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@igr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rac230.htm). For BAC library  
availability, please contact Piere de Jong (pje@jongsmaill.chi.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/orering/information.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rac/bac\_end\_intro.html  
Plate: 125 Row: M Column: 16  
Seq primer: 17  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
1..627  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SENHsd/MCM"  
/db\_xref="taxon:10116"  
/clone="CH230-125M16"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 1"  
/note="Vector: pTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CHORI-230 Rat (BN/SENHsd/MCM) BAC library produced by  
Piere de Jong"

ORIGIN  
Query Match 78.3%; Score 18.8; DB 8; Length 627;  
Best Local Similarity 90.9%; Pred. No. 3.4e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTATGTAGACAGCTCTTCAAA 23  
|||||  
322 TTATGTAGACAGCTCTTCAAA 343

Db

RESULT 10  
CL706910 632 bp DNA linear GSS 26-JUL-2004  
LOCUS OR\_BBA0024M03.r OR\_BBA Oryza rufipogon genomic clone OR\_BBA0024M03  
3', genomic survey sequence.  
ACCESSION CL706910  
VERSION CL706910.1 GI:50593948  
KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 632)  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA TAC GG  
REVERSE: TAA TAC GAC TCA TAC GG

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0024 Row: M Column: 03  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
1..632  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BBA0024M03"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBA"  
/note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
Query Match 78.3%; Score 18.8; DB 9; Length 632;  
Best Local Similarity 90.9%; Pred. No. 3.5e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TATGTAGACAGCTCTTCAAG 24  
|||||  
151 TATGTAGACAGCTCTTCAAG 172

Db

RESULT 11  
CL720267 731 bp DNA linear GSS 26-JUL-2004  
LOCUS OR\_BBA0048E12.f OR\_BBA Oryza rufipogon genomic clone OR\_BBA0048E12  
5', genomic survey sequence.  
ACCESSION CL720267  
VERSION CL720267.1 GI:50611301  
KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 731)  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA TAC GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0048 Row: E Column: 12  
Seq primer: TAA TAC GAC TCA TAC GG  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
1..731  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BBA0048E12"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBA"  
/note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
Query Match 78.3%; Score 18.8; DB 9; Length 731;  
Best Local Similarity 90.9%; Pred. No. 3.5e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TATGTAGACAGCTTTTCAAG 24  
 |||||  
 DB 151 TATGTGACTCGCTTTTCAAG 172

RESULT 12  
 CL807004/c 765 bp DNA linear GSS 09-AUG-2004  
 LOCUS OR\_CBA0020P06.f OR\_CBA Oryza rufipogon genomic clone OR\_CBA0020P06  
 DEFINITION 5', genomic survey sequence.  
 ACCESSION CL807004.1 GI:51044586  
 VERSION CL807004.1 GI:51044586  
 KEYWORDS GSS.  
 SOURCE Oryza rufipogon  
 ORGANISM Oryza rufipogon  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzae; Oryza.  
 1 (bases 1 to 765)  
 Kim, H., Yu, Y., Wisnietzki, M., Yost, D., Spum, D., Rao, K., Luo, M.,  
 Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and  
 Wang, R.  
 OMAF project  
 UNpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 PCR primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0020 row: P column: 06  
 Seq primer: TAA TAC GAC TCA CTA TAG GG  
 Class: BAC ends.  
 Location/Qualifiers  
 1..765  
 /organism="Oryza rufipogon"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4529"  
 /clone="OR\_CBA0020P06"  
 /issue\_type="young leaves"  
 /dev\_stage="2 week old seedlings"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="OR\_CBA"  
 /note="Vector: pAGIRAC1; Site\_1: HindIII; Site\_2: HindIII;  
 dir created 36 hrs before harvest"

ORIGIN

Query Match 78.3%; Score 18.8; DB 9; Length 765;  
 Best Local Similarity 90.9%; Pred. No. 3.5e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TATGTAGACAGCTTTTCAAG 24  
 |||||  
 DB 152 TATGTGACTCGCTTTTCAAG 131

RESULT 13  
 A1332619 526 bp mRNA linear EST 13-FEB-1999  
 LOCUS gq28a04.x1 Soares\_NHMPU\_S1 Homo sapiens cDNA clone IMAGE:1933806  
 DEFINITION 3' similar to SW:MP1\_RABIT\_P31429 MICROSOMAL DIPEPTIDASE PRECURSOR  
 // mRNA sequence.  
 ACCESSION A1332619  
 VERSION A1332619.1 GI:4069178  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 526)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 UNpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov.  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1131 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 412.  
 Location/Qualifiers  
 1..526  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1933806"  
 /issue\_type="Pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_NHMPU\_S1"  
 /note="Organ: mixed (see below); Vector: pT73D-Pac  
 (pharmacia) with a modified polylinker; site 1: Not I;  
 site 2: Eco RI. Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NDH, pregnant uterus  
 NDHPU, and fetal heart NDH19W) were mixed, and ss circles  
 was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from pools of  
 5,000 clones made from the same 3 libraries. The pools  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

ORIGIN

Query Match 76.7%; Score 18.4; DB 1; Length 526;  
 Best Local Similarity 95.0%; Pred. No. 5.3e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TATGTAGACAGCTTTTCA 22  
 |||||  
 DB 474 TATGTGACACGCTTTTCA 493

RESULT 14  
 BH812962 180 bp DNA linear GSS 02-MAY-2002  
 LOCUS SALK\_063510 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_063510, genomic survey sequence.  
 DEFINITION BH812962  
 ACCESSION BH812962.1 GI:20391417  
 VERSION BH812962  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 180)  
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, R., Prednis, L.,  
 Shinn, P., Zimmerman, J., and Ecker, J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 UNpublished (2001)  
 CONTACT: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 558 4100 x1752  
 Fax: 858 558 6379  
 Email: eckers@salk.edu  
 This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of  
 At3g26850.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. 180  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_063510"  
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion  
 lines each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

## ORIGIN

Query Match 75.8%; Score 18.2; DB 8; Length 180;  
 Best Local Similarity 87.0%; Pred. No. 5.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACACGCTTTCAAG 24  
 |||||  
 Db 100 TTATGTAGACAGTATGTCAAG 78

## RESULT 15

B2290962 197 bp DNA linear GSS 24-OCT-2002  
 LOCUS SALK\_112237.50.25.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_112237.50.25.x, genomic  
 survey sequence.

ACCESSION B2290962  
 VERSION B2290962.1 GI:24335370  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 197)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the

TITLE Arabidopsis Genome  
 Arabidopsis Genome  
 Unpublished (2001)

JOURNAL Contact: Joseph R. Ecker  
 COMMENT Salk Institute Genomic Analysis Laboratory (Signal)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within 300 bases of the 3' end of  
 At3g26850.  
 Class: TDNA tagged.

FEATURES  
 source  
 1. 197  
 Location/Qualifiers

/organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_112237.50.25.x"  
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

ORIGIN  
 Query Match 75.8%; Score 18.2; DB 8; Length 197;  
 Best Local Similarity 87.0%; Pred. No. 5.9e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACACGCTTTCAAG 24  
 |||||  
 Db 98 TTATGTAGACAGTATGTCAAG 76

Search completed: February 9, 2005, 21:55:30  
 Job time : 2354.9 secs

... Page Blank (uspto)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-10

Perfect score: 1 gtcctcagccacgccccgcgctg 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_Da:\*

2: gb\_Htg:\*

3: gb\_In:\*

4: gb\_Om:\*

5: gb\_Ov:\*

6: gb\_Pat:\*

7: gb\_Pn:\*

8: gb\_Pl:\*

9: gb\_Pr:\*

10: gb\_Ro:\*

11: gb\_Ats:\*

12: gb\_Sy:\*

13: gb\_Un:\*

14: gb\_Vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504307 Sequence
2	25	100.0	25	6	AX504324 Sequence
3	25	100.0	351	6	AR080196 Sequence
4	25	100.0	351	6	AR080197 Sequence
5	25	100.0	370	9	AF345623 Homo sapi
6	25	100.0	370	9	AF345624 Homo sapi
7	25	100.0	568	6	AR080195 Sequence
8	25	100.0	633	6	AX701741 Sequence
9	25	100.0	976	9	HUMMDR1A02
10	25	100.0	976	11	G19985
11	25	100.0	1318	6	AR080194 Sequence
12	25	100.0	1327	9	HUMMDR1P
13	25	100.0	1688	6	AR080193 Sequence
14	25	100.0	2090	6	AR080192 Sequence
15	25	100.0	2117	6	A38669
16	25	100.0	2186	9	HUMMDR1A
17	25	100.0	2932	6	CO806551 Sequence
18	25	100.0	2932	6	AX457064 Sequence
19	25	100.0	2932	6	AX598697 Sequence

c	20	25	100.0	2932	6	AX767353	AX767353 Sequence
c	21	25	100.0	2932	6	AX795658	AX795658 Sequence
c	22	25	100.0	2932	6	AX822109	AX822109 Sequence
c	23	25	100.0	2932	6	AX825749	AX825749 Sequence
c	24	25	100.0	2932	9	HSMDR1A	AX8723 Human MDRL
c	25	25	100.0	4553	6	CO716151	CO716151 Sequence
c	26	25	100.0	4643	6	CO815440	CO815440 Sequence
c	27	25	100.0	4643	6	AX522070	AX522070 Sequence
c	28	25	100.0	4643	6	AX587788	AX587788 Sequence
c	29	25	100.0	4646	6	BD234195	BD234195 ATP-bind
c	30	25	100.0	4646	6	CO861565	CO861565 Sequence
c	31	25	100.0	4646	6	I49610	I49610 Sequence 2
c	32	25	100.0	4646	6	AR380622	AR380622 Sequence
c	33	25	100.0	4646	6	AX336420	AX336420 Sequence
c	34	25	100.0	4646	6	AX336708	AX336708 Sequence
c	35	25	100.0	4646	6	AX310999	AX310999 Sequence
c	36	25	100.0	4646	6	AX504298	AX504298 Sequence
c	37	25	100.0	4646	9	HUMMDR1	M14758 Homo sapien
c	38	25	100.0	4669	6	AR055785	AR055785 Sequence
c	39	25	100.0	4669	6	I08557	I08557 Sequence 3
c	40	25	100.0	4669	6	AR363344	AR363344 Sequence
c	41	25	100.0	177380	6	AX706985	AX706985 Sequence
c	42	25	100.0	177380	6	AX707915	AX707915 Sequence
c	43	25	100.0	177380	9	AC002457	AC002457 Homo sapi
c	44	23.4	93.6	4669	6	AR091275	AR091275 Sequence
c	45	23.4	93.6	4669	6	AR203322	AR203322 Sequence

#### ALIGNMENTS

RESULT 1	AX504307	Sequence 10 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504307					
DEFINITION	Sequence 10 from Patent WO0234291.					
ACCESSION	AX504307					
VERSION	AX504307.1	GI:23386125				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE						
AUTHORS	Colgan, S.P.					
TITLE	Compositions and methods for treating hematologic malignancies and multiple drug resistance					
JOURNAL	Patent: WO 0234291-A 10 02-MAY-2002;					
FEATURES	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)					
SOURCE	location/Qualifiers					
ORIGIN						
Query Match	100.0%;	Score 25;	DB 6;	Length 25;		
Best Local Similarity	100.0%;	Pred. No. 41;				
Matches	25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OR	1 GTGCTCAGCCACGCCCCGCGCTG 25					
DB	1 GTGCTCAGCCACGCCCCGCGCTG 25					
RESULT 2	AX504324/c	Sequence 27 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504324					
DEFINITION	Sequence 27 from Patent WO0234291.					
ACCESSION	AX504324					
VERSION	AX504324.1	GI:23386136				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Colgan, S.P.

JOURNAL Composition and methods for treating hematologic malignancies and multiple drug resistance

FEATURES Patent: WO 0234291-A 27 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)

SOURCE Location/Qualifiers

1. 25

ORGANISM /organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCACGCGCGCGCTG 25

Db 25 GTGCTCAGCCACGCGCGCGCTG 1

RESULT 3

AR080196/c AR080196 351 bp DNA linear PAT 31-AUG-2000

LOCUS Sequence 5 from patent US 5968735.

DEFINITION AR080196

ACCESSION AR080196

VERSION AR080196.1 GI:10006931

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 351)

AUTHORS Stein, U. and Walthers, W.

JOURNAL Vector for the expression of therapy-relevant genes

FEATURES Patent: US 5968735-A 5 19-OCT-1999;

SOURCE Location/Qualifiers

1. 351

ORGANISM /organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 351;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCACGCGCGCGCTG 25

Db 170 GTGCTCAGCCACGCGCGCGCTG 146

RESULT 4

AR080197/c AR080197 351 bp DNA linear PAT 31-AUG-2000

LOCUS Sequence 6 from patent US 5968735.

DEFINITION AR080197

ACCESSION AR080197

VERSION AR080197.1 GI:10006932

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 351)

AUTHORS Stein, U. and Walthers, W.

JOURNAL Vector for the expression of therapy-relevant genes

FEATURES Patent: US 5968735-A 6 19-OCT-1999;

SOURCE Location/Qualifiers

1. 351

ORGANISM /organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 351;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCACGCGCGCGCTG 25

Db 170 GTGCTCAGCCACGCGCGCGCTG 146

RESULT 5

AF345623/c AF345623 370 bp mRNA linear PRI 02-MAY-2003

LOCUS Homo sapiens MES-SA/2B-E3 MDR1 mRNA, 5'UTR.

DEFINITION AF345623

ACCESSION AF345623

VERSION AF345623.1 GI:13591739

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 370)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL Miscellaneous notes on Pleurotus

REFERENCE 2 (bases 1 to 370)

AUTHORS Personia 18, 55-69 (2002)

JOURNAL Chen, G.-K., Wang, Y. and Sikić, B.I.

REFERENCE Direct Submission

AUTHORS Submitted (06-FEB-2001) Oncology/Medicine, Stanford University

TITLE School of Medicine, 269 Campus Drive, Stanford, CA 94305-5151, USA

FEATURES Location/Qualifiers

1. 370

ORGANISM /organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/chromosome="7"

/map="7q21.1"

/cell\_line="MES-SA/2B-E3"

/tissue\_type="uterine sarcoma"

/note="doxorubicin selected cell line"

<1..>370

/gene="MDR1"

<1..>370

/gene="MDR1"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 370;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCACGCGCGCGCTG 25

Db 250 GTGCTCAGCCACGCGCGCGCTG 226

RESULT 6

AF345624/c AF345624 370 bp mRNA linear PRI 02-MAY-2003

LOCUS Homo sapiens MES-SA/VL20-4.2 MDR1 mRNA, 5'UTR.

DEFINITION AF345624

ACCESSION AF345624

VERSION AF345624.1 GI:13591740

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 370)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL Miscellaneous notes on Pleurotus

REFERENCE 2 (bases 1 to 370)

AUTHORS Personia 18, 55-69 (2002)

JOURNAL Wang, Y., Chen, G.-K. and Sikić, B.I.

REFERENCE Direct Submission

AUTHORS Submitted (06-FEB-2001) Oncology/Medicine, Stanford University

TITLE School of Medicine, 269 Campus Drive, Stanford, CA 94305-5151, USA

School of Medicine, 269 Campus Drive, Stanford, CA 94305-5151, USA

FEATURES  
source

Location/Qualifiers  
1. .370  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="7"  
/map="7q21.1"  
/cell\_line="MES-SA/VL20-4.2"  
/tissue\_type="uterine sarcoma"  
/note="Vlnblastine selected cell line"

gene

<1. .>370  
/gene="MDR1"  
<1. .>370  
/gene="MDR1"

5'UTR

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 370;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTAGCCAGCCCGCGCGCTG 25  
|||||  
Db 250 GTGCTAGCCAGCCCGCGCGCTG 226

RESULT 7

AR080195/c 568 bp DNA linear PAT 31-AUG-2000

LOCUS AR080195 Sequence 4 from patent US 5968735.

DEFINITION AR080195

ACCESSION AR080195

VERSION AR080195.1 GI:10006930

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 568)

AUTHORS Stein, U. and Walther, W.

TITLE Vector for the expression of therapy-relevant genes

JOURNAL Patent: US 5968735-A 4 19-OCT-1999;

FEATURES Location/Qualifiers

1. .568  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 568;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTAGCCAGCCCGCGCGCTG 25  
|||||  
Db 414 GTGCTAGCCAGCCCGCGCGCTG 390

RESULT 8

AX701741/c 633 bp DNA linear PAT 03-APR-2003

LOCUS AX701741 Sequence 3 from Patent WO03002760.

DEFINITION AX701741

ACCESSION AX701741

VERSION AX701741.1 GI:29537273

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 Dietler, J. and Leu, E.

TITLE Method for detecting cytosine methylation by comparatively

JOURNAL analysing single strands of amplification

Patent: WO 03002760-A 3 09-JAN-2003;

FEATURES Epigenomics AG (DE)

Location/Qualifiers

1. .633

/organism="synthetic construct"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="MDR1-PCR-Produkt"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 633;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTAGCCAGCCCGCGCGCTG 25  
|||||  
Db 422 GTGCTAGCCAGCCCGCGCGCTG 398

RESULT 9

HUMMDR1A02/c 976 bp DNA linear PRI 08-JAN-1995

LOCUS HUMMDR1A02 Human P-glycoprotein (MDR1) gene, 5' flank.

DEFINITION M29423 J05168 M18754

ACCESSION M29423.1 GI:187472

VERSION P-glycoprotein; multidrug resistance.

KEYWORDS 2 of 26

SEGMENT

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 976)

AUTHORS Ueda, K., Pastan, I. and Gottesman, M.M.

TITLE Isolation and sequence of the promoter region of the human

JOURNAL multidrug-resistance (P-glycoprotein) gene

Ueda, K., Pastan, I. and Gottesman, M.M. and

Medline 86087023

2891692

2 (bases 1 to 976)

REFERENCE Chen, C.J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and

AUTHORS Robinson, I. B.

TITLE Genomic organization of the human multidrug resistance (MDR1) gene

JOURNAL and origin of P-glycoprotein

Ueda, K., Pastan, I. and Gottesman, M.M. and

Medline 90094448

1967175

Original source text: Human multidrug resistant cell line KB-V1

COMMENT DNA. revises [1].

Draft entry and computer-readable sequence for [1] kindly submitted

by I. B. Robinson, 27-OCT-1989.

Location/Qualifiers

1. .976  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="7q21"  
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prim\_transcript <1. .>976  
/gene="PGY1"

intron /note="PGY1 mRNA and intron (alt.); G00-120-712"

<1. .244  
/gene="PGY1"

prim\_transcript /note="PGY1, intron A"

435. .>976  
/gene="PGY1"

intron /note="PGY1 mRNA and intron (alt.)"

569. .>976  
/gene="PGY1"

intron /note="PGY1, intron A"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 976;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTAGCCAGCCCGCGCGCTG 25  
|||||

Db 400 GTGCTCAGCCACGCCGCCGCGCTG 376

RESULT 10  
LOCUS G19985/c 976 bp DNA linear STS 28-SEP-1998  
DEFINITION SMS10 Eric D. Green Homo sapiens STS genomic, sequence tagged site.

ACCESSION G19985  
VERSION G19985.1 GI:1254684  
KEYWORDS STS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 976)  
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F., Weintraub, L.A., Mohr-Ridwell, R.M., Peluso, D.C., Fulton, R.S., Leckie, M.P. and Green, E.D.  
A collection of 1814 human chromosome 7-specific STS  
Genome Res. 7 (1), 59-64 (1997)  
97189344  
9037602  
2 (bases 1 to 976)  
Green, E.D.  
Human chromosome 7 STS (1997)  
Unpublished (1997)  
SYNonyms: PGY1  
GDB: GDB:583426  
GDB DSEG: PGY1  
Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Primer A: AACGAGCCAGACATCTCC  
Primer B: AGGCTTCTGTGTCACAAAGAG  
STS size: 180  
PCR profile:

Presoak: 0 degrees C for 0.00 minute(s)  
Denaturation: 92 degrees C for 1.00 minute(s)  
Annealing: 68 degrees C for 2.00 minute(s)  
Polymerization: 72 degrees C for 2.00 minute(s)  
PCR Cycles: 35  
Thermal Cycler: PerkinElmer TC

Protocol:

Template: 30-100 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uM  
Total Vol: 5 uL

Buffer:

MgCl<sub>2</sub>: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

FEATURES  
source  
1..976  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="7"  
/clone\_lib="Eric D. Green"  
1..976  
gene

This STS was developed from sequence determined by another investigator. See GenBank record: M29423 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>. Also see Genomics 11:548-64 (1991) (MUID=92128937).  
Location/Qualifiers

STS /gene="PGY1"  
253..432  
/gene="PGY1"  
primer\_bind 253..272  
/gene="PGY1"  
complement(413..432)  
ORIGIN  
Query Match 100.0%; Score 25; DB 11; Length 976;  
Best Local Similarity 100.0%; Pred. NO. 17;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCACGCCGCCGCGCTG 25  
Db 400 GTGCTCAGCCACGCCGCCGCGCTG 376

RESULT 11  
LOCUS AR080194/c 1318 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 3 from patent US 5968735.  
ACCESSION AR080194  
VERSION AR080194.1 GI:10006929  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1318)  
Stein, U. and Walther, W.  
Vector for the expression of therapy-relevant genes  
Patent: US 5968735-A 3 19-OCT-1999;  
Location/Qualifiers  
1..1318  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 1318;  
Best Local Similarity 100.0%; Pred. NO. 16;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCACGCCGCCGCGCTG 25  
Db 1164 GTGCTCAGCCACGCCGCCGCGCTG 1140

RESULT 12  
LOCUS HUMMDR1P/c 1327 bp DNA linear PRI 09-JAN-1995  
DEFINITION Human multidrug resistant P glycoprotein (MDR1; PGY1) gene, 5' flank.  
ACCESSION L07624  
VERSION L07624.1 GI:187500  
KEYWORDS MDR1 gene; P-glycoprotein; multidrug resistance protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1327)  
Madden, M.J., Morrow, C.S., Nakagawa, M., Goldsmith, M.E., Fairchild, C.R. and Cowan, K.H.  
Identification of 5' and 3' sequences involved in the regulation of transcription of the human mdr1 gene in vivo  
J. Biol. Chem. 268 (11), 8290-8297 (1993)  
93216814  
8096520  
PUBMED  
COMMENT  
Original source text: Homo sapiens (tissue library: lambda Charon 4a) bone marrow DNA.  
Location/Qualifiers  
1..1327  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

/map="7q21"  
/cell\_type="leukocyte"  
/tissue\_type="bone marrow"  
/tissue\_lib="lambda Charon 4a"  
863..1171  
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863..875  
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/bound\_moiety="unknown"  
/function="heat shock element"  
930..937  
/gene="PGY1"  
/note="G00-120-712"  
/bound\_moiety="unknown"  
/function="heat shock element"  
930..937  
/gene="PGY1"  
/note="G00-120-712"  
/bound\_moiety="unknown"  
/function="metal responsive element"  
931..938  
/gene="PGY1"  
/note="G00-120-712"  
980..990  
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/note="G00-120-712"  
1023..1028  
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1041..>1170  
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1041..1170  
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1044..>1170  
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1050..1066  
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/note="G00-120-712"  
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/function="heat shock element"  
1171..>1171  
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intron  
ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 1327;  
Best Local Similarity 100.0%; Pred. No. 16; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GTGCTACGCCACGCCCGCGGCTG 25  
Db 1002 GTGCTACGCCACGCCCGCGGCTG 978  
RESULT 13  
AR080193/c 1688 bp DNA linear PAT 31-AUG-2000  
LOCUS AR080193 Sequence 2 from patent US 5968735.  
ACCESSION AR080193  
VERSION AR080193.1 GI:10006928  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1688)  
AUTHORS Stein,U. and Walther,W.  
TITLE Vector for the expression of therapy-relevant genes  
JOURNAL Patent: US 5968735-A 2 19-OCT-1999;  
FEATURES Location/Qualifiers  
1..1688  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 1688;  
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GTGCTACGCCACGCCCGCGGCTG 25  
Db 1534 GTGCTACGCCACGCCCGCGGCTG 1510  
RESULT 14  
AR080192/c 2090 bp DNA linear PAT 31-AUG-2000  
LOCUS AR080192 Sequence 1 from patent US 5968735.  
ACCESSION AR080192  
VERSION AR080192.1 GI:10006927  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2090)  
AUTHORS Stein,U. and Walther,W.  
TITLE Vector for the expression of therapy-relevant genes  
JOURNAL Patent: US 5968735-A 1 19-OCT-1999;  
FEATURES Location/Qualifiers  
1..2090  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 2090;  
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GTGCTACGCCACGCCCGCGGCTG 25  
Db 1936 GTGCTACGCCACGCCCGCGGCTG 1912  
RESULT 15  
A38669 2117 bp DNA linear PAT 11-NOV-1999  
LOCUS A38669/c  
DEFINITION Sequence 1 from Patent WO9411522.  
ACCESSION A38669  
VERSION A38669.1 GI:2295152  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2117)  
AUTHORS Stein,U. and Walther,W.  
TITLE VECTOR FOR THE EXPRESSION OF THERAPY-RELEVANT GENES  
JOURNAL Patent: WO 9411522-A 1 26-MAY-1994;  
MAX DELBRIECK CT FUER MOLEKULA (DE)  
Other publication DE 4238778 940519.  
COMMENT Location/Qualifiers  
1..2117  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/clone="CVS-SW1"  
/cell\_type="SARCOMAS"  
/tissue\_type="TUMORS"  
2076  
/replace="c"  
2110  
/replace="c"  
variation  
variation  
ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 2117;  
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;

Matches	25;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GTGCTCAGCCCGCCCGGCGCTG	25						
Db	1936	GTGCTCAGCCCGCCCGGCGCTG	1912						

Search completed: February 9, 2005, 17:01:54  
 Job time : 482.178 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01, Search time 78.592 Seconds  
(without alignments)  
520.498 Million cell updates/sec

Title: US-10-007-255-10  
Perfect score: 1 gtcgcagccaccccgccgctg 25  
Sequence: 4: /cgnt2\_6/ptodata/1/ina/6A COMB.seq.\*

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapex 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents, NA.\*  
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3: /cgnt2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgnt2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgnt2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgnt2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	25	100.0	US-08-439-814-5	Sequence 5, Appli
2	25	100.0	US-08-439-814-6	Sequence 6, Appli
3	25	100.0	US-08-439-814-4	Sequence 4, Appli
4	25	100.0	US-08-439-814-3	Sequence 3, Appli
5	25	100.0	US-08-439-814-2	Sequence 2, Appli
6	25	100.0	US-08-439-814-1	Sequence 1, Appli
7	25	100.0	US-09-023-655-1167	Sequence 1167, Ap
8	25	100.0	US-08-023-655-1167	Sequence 1167, Ap
9	25	100.0	US-08-583-276-18	Sequence 18, Appli
10	25	100.0	5206352-3	Patent No. 5206352
11	25	100.0	5206352-3	Patent No. 5206352
12	23.4	93.6	US-08-752-447-1	Sequence 1, Appli
13	23.4	93.6	US-09-316-167-1	Sequence 1, Appli
14	23.4	93.6	US-09-397-233-1	Sequence 1, Appli
15	20	80.0	US-08-487-141B-2	Sequence 2, Appli
16	20	80.0	US-08-927-561-2	Sequence 2, Appli
17	20	80.0	US-09-902-540-1166	Sequence 1166, Ap
18	19.4	77.6	US-09-902-540-1166	Sequence 1166, Ap
19	19.4	77.6	US-09-902-540-1179	Sequence 1179, Ap
20	18.6	74.4	US-09-513-999C-13841	Sequence 13841, A
21	18.6	74.4	US-09-949-016-174342	Sequence 174342,
22	18.6	74.4	US-09-949-016-174342	Sequence 174342,
23	18.6	74.4	US-08-311-731A-122	Sequence 122, App
24	18.6	74.4	US-09-949-016-16674	Sequence 16674, A
25	18.6	74.4	US-09-949-016-16675	Sequence 16675, A
26	18.6	74.4	US-07-626-618A-1	Sequence 1, Appli
27	18.2	72.8	US-07-626-618A-1	Sequence 1, Appli

28	18.2	72.8	388	1	US-07-928-611-1	Sequence 1, Appli
29	18.2	72.8	388	2	US-08-333-977-1	Sequence 1, Appli
30	18.2	72.8	388	2	US-08-487-811A-1	Sequence 1, Appli
31	18.2	72.8	388	3	US-09-060-694-1	Sequence 1, Appli
32	18.2	72.8	388	3	US-09-378-074-1	Sequence 1, Appli
33	18.2	72.8	388	5	PCT-US93-07370-1	Sequence 1, Appli
34	18.2	72.8	388	5	US-08-475-742-3	Sequence 3, Appli
35	18.2	72.8	388	4	US-08-261-293-3	Sequence 3, Appli
36	18.2	72.8	388	1	US-08-056-051-1	Sequence 1, Appli
37	18.2	72.8	388	1	US-07-928-611-17	Sequence 17, Appli
38	18.2	72.8	388	2	US-08-487-811A-17	Sequence 17, Appli
39	18.2	72.8	388	3	US-09-060-694-17	Sequence 17, Appli
40	18.2	72.8	388	3	US-09-378-074-17	Sequence 17, Appli
41	18.2	72.8	388	5	PCT-US93-07370-17	Sequence 17, Appli
42	18.2	72.8	388	1	US-08-056-051-3	Sequence 3, Appli
43	18.2	72.8	388	1	US-07-928-611-19	Sequence 19, Appli
44	18.2	72.8	388	2	US-08-487-811A-19	Sequence 19, Appli
45	18.2	72.8	388	3	US-09-060-694-19	Sequence 19, Appli

## ALIGNMENTS

RESULT 1  
US-08-439-814-5/c  
Sequence 5, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:  
APPLICANT: STEIN, Ulrike  
APPLICANT: WALTHER, Wolfgang  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
TITLE OF INVENTION: THERAPY-RELEVANT GENES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
STREET: Street Lobby  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439, 814  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B (ERO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE93/01086

FILED DATE: 10-NOV-1993  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-439-814-5

Query Match 100.0%; Score 25; DB 2; Length 351;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCGCCCGGCGCTG 25  
DB 170 GTGCTCAGCCCGCCCGGCGCTG 146

## RESULT 2

US-08-439-814-6/c  
Sequence 6, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:  
APPLICANT: STEIN, Ulrike  
APPLICANT: WALTHER, Wolfgang  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
TITLE OF INVENTION: THERAPY-RELEVANT GENES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,814  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
SEQUENCE CHARACTERISTICS:  
INFORMATION FOR SEQ ID NO: 6:  
LENGTH: 351 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-439-814-6

Query Match 100.0%; Score 25; DB 2; Length 351;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCGCCCGGCGCTG 25  
DB 170 GTGCTCAGCCCGCCCGGCGCTG 146

## RESULT 3

US-08-439-814-4/c  
Sequence 4, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:  
APPLICANT: STEIN, Ulrike  
APPLICANT: WALTHER, Wolfgang  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
TITLE OF INVENTION: THERAPY-RELEVANT GENES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,814  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
SEQUENCE CHARACTERISTICS:  
INFORMATION FOR SEQ ID NO: 4:  
LENGTH: 568 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)



US-08-439-814-4

Query Match 100.0%; Score 25; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCCAGCCCCGCGCTG 25  
DB 414 GTGCTAGCCCCAGCCCCGCGCTG 390

RESULT 4  
US-08-439-814-3/C  
Sequence 3, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:

APPLICANT: STEIN, Ulrike  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
TITLE OF INVENTION: THERAPY-RELEVANT GENES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,814  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1318 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-439-814-3

Query Match 100.0%; Score 25; DB 2; Length 1318;  
Best Local Similarity 100.0%; Pred. No. 0.87;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCCAGCCCCGCGCTG 25  
DB 1164 GTGCTAGCCCCAGCCCCGCGCTG 1140

RESULT 5  
US-08-439-814-2/C  
Sequence 2, Application US/08439814  
Patent No. 5968735  
GENERAL INFORMATION:

APPLICANT: STEIN, Ulrike  
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
TITLE OF INVENTION: THERAPY-RELEVANT GENES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,814  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4238778.7  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE93/01086  
FILING DATE: 10-NOV-1993  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1688 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-439-814-2

Query Match 100.0%; Score 25; DB 2; Length 1688;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1534 GTGCTCAGCCACGCCCGCGCTG 1510

## RESULT 6

US-08-439-814-1/c  
; Sequence 1, Application US/08439814  
; Patent No. 5968735  
; GENERAL INFORMATION:  
; APPLICANT: STEIN, Ullike  
; APPLICANT: WALTHER, Wolfgang  
; TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
; TITLE OF INVENTION: THERAPY-RELEVANT GENES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIKAIKO, MARIELESTEIN, MURRAY & ORAM LLP  
; STREET: 655 Fifteenth Street, N. W., Suite 330 G  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439, 814  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 4238778.7  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE PCT/DE93/01086  
; FILING DATE: 10-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KLESNER, Sharon N.  
; REGISTRATION NUMBER: 36,335  
; REFERENCE/DOCKET NUMBER: P1614-5015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/638-5000  
; TELEFAX: 202/638-4810  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4238778.7  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DE93/01086  
; FILING DATE: 10-NOV-1993  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2090 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-439-814-1

Query Match 100.0%; Score 25; DB 2; Length 2090;

Best Local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1936 GTGCTCAGCCACGCCCGCGCTG 1912

## RESULT 7

US-08-181-471-2/c

; Sequence 2, Application US/08181471  
; Patent No. 5641508  
; GENERAL INFORMATION:  
; APPLICANT: Li, Lingna  
; APPLICANT: Lishko, Valeryi K.  
; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL  
; TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Thomas Fitting  
; STREET: 12526 High Bluff Drive, Suite 300  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92130  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/181,471  
; FILING DATE: 13-JAN-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/041,553  
; FILING DATE: 02-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: ANT0029P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-792-3680  
; TELEFAX: 619-792-8477  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4646 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 425..4267  
; US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;

Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 251 GTGCTCAGCCACGCCCGCGCTG 227

## RESULT 8

US-09-023-655-1167/c  
; Sequence 1167, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cooke, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO

STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 845-4166  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4646 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g187468  
US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCAGCCGCGGCGCTG 25  
|||  
DB 251 GTGCTCAGCCAGCCGCGGCGCTG 227

RESULT 9  
US-08-583-276-18/c  
Sequence 18, Application US/08583276  
Patent No. 5837536  
GENERAL INFORMATION:  
APPLICANT: McDonagh, Kevin T.  
APPLICANT: Menhais, Arthur  
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Carella, Byrne, Baln, Gillfillan,  
ADDRESSER: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DW4.V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,276  
FILING DATE: 05-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/332,444  
FILING DATE: 31-OCT-1994  
APPLICATION NUMBER: 07/887,712  
FILING DATE: 22-MAY-1992  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 bases  
TYPE: nucleic acid  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: Genomic DNA  
US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCAGCCGCGGCGCTG 25  
|||  
DB 251 GTGCTCAGCCAGCCGCGGCGCTG 227

RESULT 10  
5206352-3/c  
Patent No. 5206352  
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,  
Michael M.  
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/622,836  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 892,575  
FILING DATE: 01-AUG-1986  
APPLICATION NUMBER: 845,610  
FILING DATE: 28-MAR-1986  
SEQ ID NO: 3;  
LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCAGCCGCGGCGCTG 25  
|||  
DB 251 GTGCTCAGCCAGCCGCGGCGCTG 227

RESULT 11  
5206352-3/c  
Patent No. 5206352  
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,  
Michael M.  
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/622,836  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 892,575  
FILING DATE: 01-AUG-1986  
APPLICATION NUMBER: 845,610  
FILING DATE: 28-MAR-1986  
SEQ ID NO: 3;  
LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;

Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTACGCCACGCCCGGCGCTG 25  
Db 251 GTGCTACGCCACGCCCGGCGCTG 227

## RESULT 12

US-08-752-447-1/c  
Sequence 1, Application US/08752447  
Patent No. 5994088  
GENERAL INFORMATION:  
APPLICANT: Mechtner, Eugene  
APPLICANT: Roninson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,447  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5994088nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-9808

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669

US-08-752-447-1

Query Match 93.6%; Score 23.4; DB 2; Length 4669;  
Best Local Similarity 96.0%; Pred. No. 3.3;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCTACGCCACGCCCGGCGCTG 25  
Db 251 GCGCTACGCCACGCCCGGCGCTG 227

RESULT 13  
US-09-316-167-1/c  
Sequence 1, Application US/09316167  
Patent No. 6365357  
GENERAL INFORMATION:

APPLICANT: Mechtner, Eugene  
APPLICANT: Roninson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/316,167  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752,447  
FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:  
NAME: No. 6365357nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-9808

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669

US-09-316-167-1

Query Match 93.6%; Score 23.4; DB 3; Length 4669;  
Best Local Similarity 96.0%; Pred. No. 3.3;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCTACGCCACGCCCGGCGCTG 25  
Db 251 GCGCTACGCCACGCCCGGCGCTG 227

## RESULT 14

US-09-397-233-1/c  
Sequence 1, Application US/09397233  
Patent No. 6630327  
GENERAL INFORMATION:  
APPLICANT: Mechtner, Eugene  
APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois

COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/397,233  
FILING DATE: 16-Sep-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6630327nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-397-233-1  
Query Match 93.6%; Score 23.4; DB 4; Length 4669;  
Best Local Similarity 96.0%; Pred. No. 3.3;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GTGCTCAGCCCAAGCGGCGGCTG 25  
DB 251 GCGCTCAGCCCAAGCGGCGGCTG 227  
RESULT 15  
US-08-487-141B-2  
Sequence 2, Application US/08487141B  
Patent No. 5683987  
GENERAL INFORMATION:  
APPLICANT: Smith, Larry J.  
TITLE OF INVENTION: Therapeutic Oligonucleotides  
TITLE OF INVENTION: Targeting the Human MDR1 and MRP Genes  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,141B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,180

FILING DATE: 12-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hagan, Patrick J.  
REGISTRATION NUMBER: 27,643  
REFERENCE/DOCKET NUMBER: 63082C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215)563-4100  
TELEFAX: (215)563-4044  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-487-141B-2  
Query Match 80.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 20; Conservative 0; Mismatches 0;  
QY 1 GTGCTCAGCCCAAGCGGCGG 20  
DB 1 GTGCTCAGCCCAAGCGGCGG 20  
Search completed: February 9, 2005, 17:11:14  
Job time : 79.592 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds  
(without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-10

Perfect score: 1 gtcgtcagccacgccccgcctg 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

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12: /cgn2\_6/ptodaca/1/pubpna/US10C\_PUBCOMB.seq:\*  
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15: /cgn2\_6/ptodaca/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodaca/1/pubpna/US10C\_PUBCOMB.seq:\*  
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20: /cgn2\_6/ptodaca/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodaca/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodaca/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	25	100.0	633	18	US-10-482-433A-3
C 2	25	100.0	2307	9	US-09-805-020-31
C 3	25	100.0	2932	18	US-10-473-126-37
C 4	25	100.0	4533	9	US-09-805-020-30
C 5	25	100.0	4643	13	US-10-072-621-2
C 6	25	100.0	4643	14	US-10-097-340-1
C 7	25	100.0	4643	15	US-10-007-926A-258
C 8	25	100.0	4646	11	US-09-968-007A-459
C 9	25	100.0	4646	11	US-09-968-007A-747
C 10	25	100.0	4646	17	US-10-641-643-1167
C 11	25	100.0	4646	17	US-10-343-657-1

	C 12	25	100.0	4646	18	US-10-775-169-198	Sequence 198, App
	C 13	23.4	93.6	4669	18	US-10-680-516-1	Sequence 1, Appl
	C 14	19.2	76.8	2692	9	US-09-880-107-3828	Sequence 3828, Ap
	C 15	19.2	76.8	2692	11	US-09-968-007A-755	Sequence 755, App
	C 16	18.6	74.4	556	9	US-09-864-761-13425	Sequence 13425, A
	C 17	18.6	74.4	604	18	US-10-357-930-56850	Sequence 56850, A
	C 18	18.6	74.4	706	18	US-10-767-701-5342	Sequence 5342, Ap
	C 19	18.6	74.4	6073	13	US-10-024-623-16	Sequence 16, Appl
	C 20	18.6	74.4	6073	15	US-10-154-419-66	Sequence 61, Appl
	C 21	18.6	74.4	6073	16	US-10-146-733-61	Sequence 12083, A
	C 22	18.4	73.6	867	18	US-10-437-963-12083	Sequence 17493, A
	C 23	18.4	73.6	4446	17	US-10-282-122A-17493	Sequence 544, App
	C 24	18.4	73.6	28049	18	US-10-322-281-544	Sequence 63236, A
	C 25	18.2	72.8	333	14	US-10-425-115-63236	GENERAL INFORMAT
	C 26	18.2	72.8	388	18	US-10-324-260-1	Sequence 7696, Ap
	C 27	18.2	72.8	504	16	US-10-029-386-7696	Sequence 8299, Ap
	C 28	18.2	72.8	602	18	US-10-767-701-8299	Sequence 6, Appl
	C 29	18.2	72.8	633	18	US-10-482-433A-6	Sequence 164589,
	C 30	18.2	72.8	750	13	US-10-027-632-164589	Sequence 164589,
	C 31	18.2	72.8	750	17	US-10-027-632-164589	Sequence 31550, A
	C 32	18.2	72.8	1250	17	US-10-425-114-31550	Sequence 3, Appl
	C 33	18.2	72.8	1367	15	US-10-241-313-3	Sequence 17, Appl
	C 34	18.2	72.8	1370	14	US-10-224-260-17	Sequence 19, Appl
	C 35	18.2	72.8	1466	14	US-10-224-260-19	Sequence 21, Appl
	C 36	18.2	72.8	1610	14	US-10-224-260-21	Sequence 28838, A
	C 37	18.2	72.8	1763	17	US-10-425-114-28838	Sequence 31892, A
	C 38	18.2	72.8	1763	17	US-10-437-963-72302	Sequence 72302, A
	C 39	18.2	72.8	1818	18	US-10-302-172-845	Sequence 845, App
	C 40	18.2	72.8	2128	17	US-09-738-626-845	Sequence 273, App
	C 41	18.2	72.8	2325	9	US-10-494-674-85	Sequence 85, Appl
	C 42	18.2	72.8	2325	18	US-10-425-115-150283	Sequence 150283,
	C 43	18.2	72.8	2383	18	US-10-092-900A-153	Sequence 153, App
	C 44	18.2	72.8	2580	17	US-10-052-586-575	Sequence 575, App
	C 45	18.2	72.8	2738	13		

#### ALIGNMENTS

RESULT 1  
US-10-482-433A-3/c  
; Sequence 3, Application US/10482433A  
; Publication No. US2004026581A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative  
; FILE REFERENCE: 82174  
; CURRENT FILING DATE: 2003-12-29  
; PRIOR APPLICATION NUMBER: DE 10132212.7  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent version 3.2  
; SEQ ID NO 3  
; LENGTH: 633  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amplification Product of MdRI-Fragment  
US-10-482-433A-3

Query Match 100.0%; Score 25; DB 18; Length 633;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCACGCGCGCGCTG 25

DB 422 GTGCTCAGCCACGCGCGCGCTG 398

RESULT 2  
US-09-805-020-31/c

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; Sequence 31, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2307)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-31
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Query Match          100.0%; Score 25; DB 9; Length 2307;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GTGCTCAGCCCGCCCGCGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGCGCGCTG 227
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RESULT 3
US-10-473-126-37/c
; Sequence 37, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
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; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 37
; LENGTH: 2932
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-473-126-37
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Query Match          100.0%; Score 25; DB 18; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GTGCTCAGCCCGCCCGCGCGCTG 25
Db      1039 GTGCTCAGCCCGCCCGCGCGCTG 1015
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RESULT 4
US-09-805-020-30/c
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; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1)..(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30
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Query Match          100.0%; Score 25; DB 9; Length 4533;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GTGCTCAGCCCGCCCGCGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGCGCGCTG 227
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RESULT 5
US-10-072-621-2/c
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; Sequence 2, Application US/10072621
; Publication No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Connop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF ANYLOID PRECURSOR PROTEIN EXPRESSION
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-2
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Query Match          100.0%; Score 25; DB 13; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GTGCTCAGCCCGCCCGCGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGCGCGCTG 227
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RESULT 6
US-10-097-340-1/c
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; Sequence 1, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHWANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
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; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-097-340-1

Query Match      100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227

RESULT 7
US-10-007-926A-258/C
; Sequence 258, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUJAGATE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: acp-binding cassette, sub-family b
; OTHER INFORMATION: (mdr/cap), member 1 (ABCB1) gene.
; US-10-007-926A-258

Query Match      100.0%; Score 25; DB 15; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227

RESULT 8
US-09-968-007A-459/C
; Sequence 459, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
```

```

; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 459
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-968-007A-459

Query Match      100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227

RESULT 9
US-09-968-007A-747/C
; Sequence 747, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 747
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-968-007A-747

Query Match      100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227
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RESULT 10  
US-10-641-643-1167/c  
; Sequence 1167, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocke, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1167:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4646 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9187468  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :  
US-10-641-643-1167  
Query Match 100.0%; Score 25; DB 17; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227  
RESULT 11  
US-10-343-657-1/c  
; Sequence 1, Application US/10343657  
; Publication No. US20040086882A1  
; GENERAL INFORMATION:  
; APPLICANT: Roninson, Igor B.  
; APPLICANT: Ruth, Adam  
; TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its  
; TITLE OF INVENTION: Ability to confer Resistance to Chemotherapeutic Drugs  
; FILE REFERENCE: 00,616-A  
; CURRENT APPLICATION NUMBER: US/10/343,657  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/222,313  
; PRIOR FILING DATE: 2000-08-01  
; NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1  
; LENGTH: 4646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (425)..(4264)  
US-10-343-657-1  
Query Match 100.0%; Score 25; DB 17; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227  
RESULT 12  
US-10-775-169-198/c  
; Sequence 198, Application US/10775169  
; Publication No. US20040175743A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dornier, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities in Vivo  
; FILE REFERENCE: AML01080 (031896-013000)  
; CURRENT APPLICATION NUMBER: US/10/775,169  
; CURRENT FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 5278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 198  
; LENGTH: 4646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-775-169-198  
Query Match 100.0%; Score 25; DB 18; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227  
RESULT 13  
US-10-680-516-1/c  
; Sequence 1, Application US/10680516  
; Publication No. US20040166110A1  
; GENERAL INFORMATION:  
; APPLICANT: Mechevner, Eugene  
; Roninson, Igor B  
; TITLE OF INVENTION: Methods and Reagents for Preparing and  
; Using Immunological Agents Specific for P-glycoprotein  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
; STREET: 300 South Wacker Drive, Seventh Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

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      APPLICATION NUMBER: US/10/680,516
      FILING DATE: 07-Oct-2003
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/752,447
      FILING DATE: 15-NOV-1996
      ATTORNEY/AGENT INFORMATION:
      NAME: Noonan, Kevin E
      REGISTRATION NUMBER: 35,303
      REFERENCE/DOCKET NUMBER: 95,1121
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 312-913-0001
      TELEFAX: 312-913-9808
      INFORMATION FOR SEQ ID NO: 1:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 4669 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: CDNA
      FEATURE:
      NAME/KEY: 5'UTR
      LOCATION: 1..424
      NAME/KEY: CDS
      LOCATION: 425..4264
      FEATURE:
      NAME/KEY: 3'UTR
      LOCATION: 4265..4669
      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-680-516-1

Query Match      93.6%; Score 23.4; DB 18; Length 4669;
Best Local Similarity 96.0%; Pred. No. 0.65;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTGCTAGCCAGCCCGCGGCGCTG 25
      |||||||
Db      251 GCGCTAGCCAGCCAGCCCGCGGCGCTG 227

RESULT 14
US-09-880-107-3828/c
; Sequence 3828, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-MO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3828
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X94563
US-09-880-107-3828

Query Match      76.8%; Score 19.2; DB 9; Length 2692;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GTGCTAGCCAGCCCGCGGCGCT 24
```

```

      |||||
Db      1083 GTGCCAGCCCGCGCGGCGGCT 1060

RESULT 15
US-09-968-007A-755/c
; Sequence 755, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 755
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-755

Query Match      76.8%; Score 19.2; DB 11; Length 2692;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GTGCTAGCCAGCCCGCGGCGCT 24
      |||||||
Db      1083 GTGCCAGCCCGCGCGGCGGCT 1060

Search completed: February 9, 2005, 22:26:36
Job time : 267.667 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds  
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Title: US-10-007-255-10

Perfect score: 1 gtgtctagccacgccccgcctcg 25

Scoring table: IDENTITY NUC  
Gapop 10'-0, Gapexc 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6 AAD39009	Aad39009 Human mdr
2	25	100.0	25	6 AAD38999	Aad38999 Human mdr
3	25	100.0	52	10 ABV75271	ABV75271 hMDR1 pro
4	25	100.0	52	10 ABV75270	ABV75270 hMDR1 pro
5	25	100.0	56	10 ABV75282	ABV75282 C3 dimer
6	25	100.0	56	10 ABV75276	ABV75276 C3mut1 co
7	25	100.0	56	10 ABV75272	ABV75272 C3mut1 co
8	25	100.0	60	10 ABV75283	ABV75283 C3 dimer
9	25	100.0	60	10 ABV75277	ABV75277 C3mut3 co
10	25	100.0	60	10 ABV75273	ABV75273 C3mut1 co
11	25	100.0	424	13 ADR12342	ADR12342 Human P-9
12	25	100.0	568	2 AAG62615	AAG62615 Human mdr
13	25	100.0	633	8 ABX94595	ABX94595 Human mdr
14	25	100.0	1024	10 ABZ83718	ABZ83718 Toxicolog
15	25	100.0	1318	2 AAG62614	AAG62614 Human mdr
16	25	100.0	1688	2 AAG62613	AAG62613 Human mdr
17	25	100.0	2090	2 AAG62612	AAG62612 Human mdr
18	25	100.0	2307	6 ABG55230	ABG55230 cDNA enco
19	25	100.0	2932	8 ABZ09897	ABZ09897 Human 5'
20	25	100.0	2932	10 ADB53945	ADB53945 MDR1 geno

21	25	100.0	2932	10 ADE84005	AdE84005 5' regula
22	25	100.0	2932	13 ADS88985	AdS88985 Human ABC
23	25	100.0	4533	6 ABS65229	ABS65229 cDNA enco
24	25	100.0	4643	6 ABS76358	ABs76358 cDNA enco
25	25	100.0	4643	6 ABV94267	ABv94267 Breast ca
26	25	100.0	4643	6 ABV74349	ABv74349 Human ABC
27	25	100.0	4643	10 ABX77217	ABx77217 cDNA enco
28	25	100.0	4643	12 ADP18689	ADp18689 Human MDR
29	25	100.0	4643	12 ADO19748	ADo19748 Human PRO
30	25	100.0	4643	13 ADP54881	ADp54881 Human PRO
31	25	100.0	4646	2 AAQ72872	AAq72872 Human mul
32	25	100.0	4646	3 AAZ94738	AAz94738 Human ATP
33	25	100.0	4646	6 ABL68592	ABl68592 Kidney ca
34	25	100.0	4646	6 ABL68880	ABl68880 Kidney ca
35	25	100.0	4646	6 AAD38994	AdD38994 Human mdr
36	25	100.0	4646	10 ADK60994	ADk60994 Ovarian c
37	25	100.0	4646	11 ADI31841	ADi31841 Human CDN
38	25	100.0	4646	13 ADR52847	ADr52847 Drug cher
39	25	100.0	4669	1 AAAT70752	AAAT70752 Sequence
40	25	100.0	4669	2 AAO52726	AAQ52726 Sequence
41	25	100.0	5544	13 ACN43504	ACn43504 Human dia
42	25	100.0	8573	6 ABS98184	ABs98184 Human mul
43	25	100.0	10200	6 AAD41243	AdA41243 Human MDR
44	25	100.0	177380	8 ACF62751	ACf62751 Cancer ba
45	25	100.0	177380	8 ADB20870	ADb20870 MRP1 base

## ALIGNMENTS

RESULT 1	
AAD39009/c	
ID AAD39009 standard; DNA; 25 BP.	
XX	
AC AAD39009;	
DT 23-SEP-2002 (first entry)	
XX	
DE Human mdr1 gene HIF-1 binding site DNA #2.	
XX	
DE Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;	
KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;	
KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;	
KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;	
KW angigenic myeloid metaplasia; myeloid leukaemia; gene therapy;	
KW polycythaemia vera; hypoxia responsive element; HRE; ds.	
XX	
OS Homo sapiens.	
XX	
PH Key	Location/Qualifiers
FT misc_binding	11..15
FT	/*tag= a
FT	/bound_molecly= "HIF-1"
XX	
PN WO200234291-A2.	
XX	
PD 02-MAY-2002.	
XX	
PF 25-OCT-2001; 2001WO-US049856.	
XX	
PR 26-OCT-2000; 2000US-0243542P.	
XX	
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.	
XX	
PI Colgan SP;	
XX	
DR WPI; 2002-471427/50.	
XX	
PT Treating a subject (at risk of) having a hematologic malignancy or	
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia	
PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1	
PT binding molecules.	
XX	

PS Example 2; Page 12; 92pp; English.  
 XX  
 CC The invention relates to a method of treating a subject having or at risk  
 CC of developing a haematologic malignancy or multidrug resistance (MDR).  
 CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
 CC binding molecules or small ubiquitin-like modifier (SUMO)-1 binding  
 CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive  
 CC element (HRE) binding molecules or antisense nucleic acid molecules and  
 CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
 CC subject having or at risk of developing haematologic malignancy or MDR  
 CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
 CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
 CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
 CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia  
 CC myeloid metaplasia, essential thrombocythemia or polycythemia vera. The  
 CC invention is used in gene therapy. The present sequence is human mdr1  
 CC gene HIF-1 binding site DNA  
 CC  
 SQ Sequence 25 BP; 3 A; 8 C; 12 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Gaps 0;  
 Matches 25; Conservative 0; Indels 0; Gaps 0;  
 Qy 1 GTGCTCAGCCCAAGCCCGCGCTG 25  
 Db 25 GTGCTCAGCCCAAGCCCGCGCTG 1  
 RESULT 2  
 AAD38999  
 ID AAD38999 standard; DNA; 25 BP.  
 AC AAD38999;  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human mdr1-HRE antisense oligonucleotide #2.  
 XX  
 KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;  
 KW hypoxia inducible factor-1; small ubiquitin-like modifier; HIF-1;  
 KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
 KW myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma;  
 KW angioleukemia; myeloid metaplasia; myeloid leukaemia; gene therapy;  
 KW polycythemia vera; hypoxia responsive element; HRE; antisense;  
 KW phosphorothioate backbone; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..25  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT  
 XX  
 PN WO200234291-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 25-OCT-2001; 2001MO-US049856.  
 XX  
 PR 26-OCT-2000; 2000US-0243542P.  
 XX  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 XX  
 PI Colgan SB;  
 XX  
 DR WPI; 2002-471427/50.  
 XX  
 PT Treating a subject (at risk of) having a hematologic malignancy or  
 PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia  
 PT inducible factor 1 binding molecules or small ubiquitin-like modifier-1

PT binding molecules.  
 XX  
 PS Claim 14; Page 43; 92pp; English.  
 XX  
 CC The invention relates to a method of treating a subject having or at risk  
 CC of developing a haematologic malignancy or multidrug resistance (MDR).  
 CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
 CC binding molecules or small ubiquitin-like modifier (SUMO)-1 binding  
 CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive  
 CC element (HRE) binding molecules or antisense nucleic acid molecules and  
 CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
 CC subject having or at risk of developing haematologic malignancy or MDR  
 CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
 CC include lymphocytic leukemia or chronic lymphoproliferative disorders  
 CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
 CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia  
 CC myeloid metaplasia, essential thrombocythemia or polycythemia vera. The  
 CC invention is used in gene therapy. The present sequence is an antisense  
 CC oligo targeted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its  
 CC expression. This oligo is used in the exemplification of the invention  
 CC  
 SQ Sequence 25 BP; 2 A; 12 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTGCTCAGCCCAAGCCCGCGCTG 25  
 Db 1 GTGCTCAGCCCAAGCCCGCGCTG 25  
 RESULT 3  
 ABV75271  
 ID ABV75271 standard; DNA; 52 BP.  
 AC ABV75271;  
 DT 07-MAR-2003 (first entry)  
 XX  
 DE hMDR1 promoter element containing antisense oligonucleotide.  
 XX  
 KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;  
 KW immediate early gene; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200279470-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002MO-US009882.  
 XX  
 PR 30-MAR-2001; 2001US-0280211P.  
 XX  
 PA (KING/) KING A C.  
 XX  
 PI King AC;  
 XX  
 DR WPI; 2003-103274/09.  
 XX  
 PT New promoter chimera useful for in vivo or in vitro expression comprises  
 PT viral promoter, intron or other transcription regulatory elements and  
 PT disease-specific promoter, intron or other transcription regulatory  
 PT sequences.  
 XX  
 PS Example 1; Page 20; 48pp; English.  
 XX  
 CC The invention relates to a new promoter chimera for in vivo or in vitro  
 CC expression that comprises: (a) a viral promoter, intron or other unit  
 CC transcription regulatory sequence of any length; and (b) a unit disease-  
 CC specific promoter, intron or other unit transcription regulatory sequence  
 CC of any length sensitive to genotoxic stress. The promoter chimera, and

vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved expression constructs for in vitro and in vivo expression of therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter chimeras of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the activity of promoter chimera

Sequence 52 BP; 7 A; 25 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTCAGCCAGCCCGGCGCTG 25  
3 GTGCTCAGCCAGCCCGGCGCTG 27

## RESULT 4

ABV75270/c  
ID ABV75270 standard; DNA; 52 BP.

ABV75270;

07-MAR-2003 (first entry)

hMDR1 promoter element containing sense oligonucleotide.

Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;

Immediate early gene; gene therapy; ss.

Synthetic.

W0200279470-A1.

10-OCT-2002.

29-MAR-2002; 2002WO-US009882.

30-MAR-2001; 2001US-0280211P.

(KING/) KING A C.

KING AC;

WPI; 2003-103274/09.

New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory sequences.

Example 1; Page 20; 48bp; English.

The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter chimeras of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the activity of promoter chimera

Sequence 52 BP; 9 A; 11 C; 25 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTCAGCCAGCCCGGCGCTG 25  
50 GTGCTCAGCCAGCCCGGCGCTG 26

## RESULT 5

ABV75282/c  
ID ABV75282 standard; DNA; 56 BP.

ABV75282;

07-MAR-2003 (first entry)

C3 dimer and trimer constructs creating sense oligonucleotide.

Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;

Immediate early gene; gene therapy; ss.

Synthetic.

W0200279470-A1.

10-OCT-2002.

29-MAR-2002; 2002WO-US009882.

30-MAR-2001; 2001US-0280211P.

(KING/) KING A C.

KING AC;

WPI; 2003-103274/09.

New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory sequences.

Example 1; Page 21; 48bp; English.

The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter chimeras of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the activity of promoter chimera

Sequence 56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTCAGCCAGCCCGGCGCTG 25  
51 GTGCTCAGCCAGCCCGGCGCTG 27

## RESULT 6

```

ABV75276/c
ID ABV75276 standard; DNA; 56 BP.
XX
AC ABV75276;
XX
DT 07-MAR-2003 (first entry)
XX
DE C3mut3 construct creating sense oligonucleotide.
XX
KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
KM immediate early gene; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX
PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX
PS Example 1; Page 21; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC expression constructs for in vitro and in vivo expression of
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCMV IE sequences not contributing to the
CC activity of promoter chimera
XX
SQ Sequence 56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTCAGCCACGCCCGCGCTG 25
DB 51 GTGCTCAGCCACGCCCGCGCTG 27

```

```

XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX
PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX
PS Example 1; Page 20; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC expression constructs for in vitro and in vivo expression of
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCMV IE sequences not contributing to the
CC activity of promoter chimera
XX
SQ Sequence 56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTCAGCCACGCCCGCGCTG 25
DB 27 GTGCTCAGCCACGCCCGCGCTG 3

```



PA (KING/) KING A C.  
XX  
XX King AC;  
XX  
XX WPI; 2003-103274/09.  
XX  
XX New promoter chimera useful for in vivo or in vitro expression comprises  
PT viral promoter, intron or other transcription regulatory elements and  
PT disease-specific promoter, intron or other transcription regulatory  
PT sequences.  
XX  
XX Example 1; Page 21; 48pp; English.  
XX  
XX The invention relates to a new promoter chimera for in vivo or in vitro  
CC expression that comprises: (a) a viral promoter, intron or other unit  
CC transcription regulatory sequence of any length; and (b) a unit disease-  
CC specific promoter, intron or other unit transcription regulatory sequence  
CC of any length sensitive to genotoxic stress. The promoter chimera, and  
CC vector comprising the chimera are useful for in vivo or in vitro  
CC expression. The method is useful for the generation of improved  
CC expression constructs for in vitro and in vivo expression of  
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter  
CC chimeras of the present invention are more potent than either promoter  
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in  
CC the construction of promoter chimeras having hMDR1 disease specific DNA  
CC element and deletion of HCMV IE sequences not contributing to the  
CC activity of promoter chimera  
XX  
SQ Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 25; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GTGCTCAGCCACGCCCGCGCTG 25  
DB 6 GTGCTCAGCCACGCCCGCGCTG 30  
  
RESULT 9  
ABV75277 standard; DNA; 60 BP.  
XX  
XX ABV75277;  
XX  
XX 07-MAR-2003 (first entry)  
XX  
XX C3mut3 construct creating antisense oligonucleotide.  
XX  
XX Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;  
XX immediate early gene; gene therapy; ss.  
XX  
XX Synthetic.  
XX  
XX WO200279470-A1.  
XX  
XX 10-OCT-2002.  
XX  
XX 29-MAR-2002; 2002WO-US009882.  
XX  
XX 30-MAR-2001; 2001US-0280211P.  
XX  
XX (KING/) KING A C.  
XX  
XX King AC;  
XX  
XX WPI; 2003-103274/09.  
XX  
XX New promoter chimera useful for in vivo or in vitro expression comprises  
PT viral promoter, intron or other transcription regulatory elements and  
PT disease-specific promoter, intron or other transcription regulatory  
PT sequences.  
XX

PS Example 1; Page 21; 48pp; English.  
XX  
XX The invention relates to a new promoter chimera for in vivo or in vitro  
CC expression that comprises: (a) a viral promoter, intron or other unit  
CC transcription regulatory sequence of any length; and (b) a unit disease-  
CC specific promoter, intron or other unit transcription regulatory sequence  
CC of any length sensitive to genotoxic stress. The promoter chimera, and  
CC vector comprising the chimera are useful for in vivo or in vitro  
CC expression. The method is useful for the generation of improved  
CC expression constructs for in vitro and in vivo expression of  
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter  
CC chimeras of the present invention are more potent than either promoter  
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in  
CC the construction of promoter chimeras having hMDR1 disease specific DNA  
CC element and deletion of HCMV IE sequences not contributing to the  
CC activity of promoter chimera  
XX  
SQ Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 25; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GTGCTCAGCCACGCCCGCGCTG 25  
DB 6 GTGCTCAGCCACGCCCGCGCTG 30  
  
RESULT 10  
ABV75273 standard; DNA; 60 BP.  
XX  
XX ABV75273;  
XX  
XX 07-MAR-2003 (first entry)  
XX  
XX C3mutl construct creating antisense oligonucleotide.  
XX  
XX Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;  
XX immediate early gene; gene therapy; ss.  
XX  
XX Synthetic.  
XX  
XX WO200279470-A1.  
XX  
XX 10-OCT-2002.  
XX  
XX 29-MAR-2002; 2002WO-US009882.  
XX  
XX 30-MAR-2001; 2001US-0280211P.  
XX  
XX (KING/) KING A C.  
XX  
XX King AC;  
XX  
XX WPI; 2003-103274/09.  
XX  
XX New promoter chimera useful for in vivo or in vitro expression comprises  
PT viral promoter, intron or other transcription regulatory elements and  
PT disease-specific promoter, intron or other transcription regulatory  
PT sequences.  
XX  
XX Example 1; Page 21; 48pp; English.  
XX  
XX The invention relates to a new promoter chimera for in vivo or in vitro  
CC expression that comprises: (a) a viral promoter, intron or other unit  
CC transcription regulatory sequence of any length; and (b) a unit disease-  
CC specific promoter, intron or other unit transcription regulatory sequence  
CC of any length sensitive to genotoxic stress. The promoter chimera, and  
CC vector comprising the chimera are useful for in vivo or in vitro  
CC expression. The method is useful for the generation of improved  
CC expression constructs for in vitro and in vivo expression of  
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter

CC chimeras of the present invention are more potent than either promoter  
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in  
CC the construction of promoter chimeras having hMDR1 disease specific DNA  
CC element and deletion of HCV IE sequences not contributing to the  
CC activity of promoter chimera

XX Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
|||  
DB 30 GTGCTCAGCCCAAGCCCGGCGCTG 54

RESULT 11

ID ADR12342/c  
ADRI2342 standard; DNA; 424 BP.

XX ADR12342;

DT 21-OCT-2004 (first entry)

XX Human P-glycoprotein 5'-untranslated region DNA.

XX ss; cytosstatic; VEGF modulator; angiogenesis inhibitor;  
KW UTR-dependent expression; Vascular endothelial growth factor;  
KW untranslated region; cancer; angiogenesis.

XX Homo sapiens.

PN W02004065561-A2.

PD 05-AUG-2004.

XX 21-JAN-2004; 2004WO-US001643.

PR 21-JAN-2003; 2003US-0441637P.

PA (PTCT-) PTC THERAPEUTICS INC.

XX Cao L, Trifillis P;

XX WPI; 2004-571681/55.

PT Identifying modulators of untranslated region-dependent expression of a  
PT VEGF gene, useful for treating cancer, comprises contacting a compound  
PT with a cell or translation mixture containing a reporter gene linked to a  
PT VEGF gene UTR.

XX Example; SEQ ID NO 51; 251pp; English.

XX A method of identifying (M1) a compound that modulates untranslated  
CC region-dependent expression of a vascular endothelial growth factor  
CC (VEGF) gene comprises contacting a member of a library of compounds with  
CC a cell or cell-free translation mixture containing a reporter gene  
CC operably linked to an untranslated region (UTR) of the VEGF gene, and  
CC detecting expression of the reporter gene. A compound is identified as  
CC modulator if the level of expression of the reporter gene in the presence  
CC of the compound is altered as compared to that in the absence of the  
CC compound or in the presence of a control. Compounds identified by M1 are  
CC useful for treating, preventing or ameliorating cancer or its symptoms,  
CC and/or for inhibiting angiogenesis. This sequence corresponds to a  
CC therapeutic untranslated region used in the invention.

XX Sequence 424 BP; 99 A; 108 C; 111 G; 106 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 424;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
|||  
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227

RESULT 12  
ID AAQ62615/c  
AAQ62615 standard; DNA; 568 BP.

XX AAQ62615;

DT 25-MAR-2003 (revised)

DT 17-JAN-1995 (first entry)

DE Human mdr-1 promoter fragment.

XX inducible promoter; cytosstatic agent; adriamycin; vincristine;  
KW multiple drug resistance; mdr-1; mammalian expression vector;  
KW cancer therapy; ss.

XX Homo sapiens.

PN DE4238778-A1.

PD 19-MAY-1994.

XX 12-NOV-1992; 92DE-04238778.

PR 12-NOV-1992; 92DE-04238778.

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Stein U, Walther W;

XX WPI; 1994-168680/21.

PT New mammalian expression vector useful for gene therapy, - comprising the  
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to  
PT cytosstatic agents.

PS Claim 2; Page 6; 7pp; German.

XX This is a preferred fragment of the mdr-1 gene promoter, isolated from  
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by  
CC cytosstatic agents such as vincristine and adriamycin which are used in  
CC cancer therapy. Vectors comprising the promoter and enhancer sequences  
CC operably linked to heterologous genes coding for therapeutic agents are  
CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,  
CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the  
CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX Sequence 568 BP; 142 A; 127 C; 143 G; 156 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
|||  
DB 414 GTGCTCAGCCCAAGCCCGGCGCTG 390

RESULT 13

ID ABX94595/c  
ABX94595 standard; DNA; 633 BP.

XX ABX94595;

DT 17-JUN-2003 (first entry)

XX Human Mdr1 DNA SEQ ID 3.

KW Mdr1, cytosine methylation; hydrogen sulphite; diagnosis; dementia;  
KW 5-methylcytosine; amplification; prognosis; side effect; medication; bone;  
KW cancer; central nervous system disorder; aggression; muscle; endocrine;  
KW abnormal development; personality disorder; behavioural disorder; injury;  
KW brain damage; psychotic disorder; cardiovascular disease; infection;  
KW gastrointestinal tract; sexual malfunction; de.  
XX  
OS Homo sapiens.  
XX  
PN WO2003023760-A2.  
XX  
PD 09-JAN-2003.  
XX  
PF 27-JUN-2002; 2002WO-DE002433.  
XX  
PR 27-JUN-2001; 2001DE-01032212.  
XX  
PA (EPIC-) EPIDENOMICS AG.  
XX  
PI Diastler J, Leu E;  
XX  
PI WPI; 2003-201513/19.  
XX  
PT Determining cytosine methylation in a genomic DNA sample by treating with  
PT hydrogen sulfite and analyzing the result, to diagnose associated  
PT conditions including cancer and brain disorders.  
XX  
PS Example 1; Page 17; 38pp; German.  
XX  
CC This invention describes a novel method of determining cytosine  
CC methylation in a sample of genomic DNA which comprises treating the  
CC sample with hydrogen sulphite so that the cytosine is converted to uracil  
CC whilst 5-methylcytosine remains unchanged, amplifying sections of the DNA  
CC using at least 2 PCR primers and studying the base composition of both  
CC complementary amplified strands whereby methylation status is deduced  
CC from the difference in molecular weight of the two strands. The method is  
CC used to diagnose and/or prognosis unwanted side effects of medication,  
CC cancer, central nervous system disorders, aggression symptoms or  
CC behavioural disorders, clinical, psychological and social consequence of  
CC brain damage, psychotic and personality disorders, dementia and  
CC associated disorders, cardiovascular disease, malfunction, bone muscle,  
CC disease of the gastrointestinal tract, breathing system, damage or  
CC endocrine or metabolic system, injury, infection, abnormal development or  
CC sexual malfunction. This sequence represents the human Mdr1 DNA fragment  
CC amplified by the PCR primers represented in ABX94593 & ABX94594 and is  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 633 BP; 161 A; 143 C; 165 G; 164 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 25; DB 8; Length 633;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
DB 422 GTGCTCAGCCCAAGCCCGGCGCTG 398  
XX  
RESULT 14  
AB283718/c  
ID AB283718 standard; cDNA; 1024 BP.  
XX  
AC AB283718;  
XX  
XX 14-MAY-2003 (first entry)  
XX  
DE Toxically relevant human nucleotide sequence #877.  
XX  
KW Toxically relevant gene; toxicological response; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016500-A2.

XX  
PD 27-FEB-2003.  
XX  
XX 16-ANG-2002; 2002WO-US026514.  
XX  
PF 16-AUG-2001; 2001US-0313080P.  
XX  
PR (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
XX  
PA Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweizer K;  
XX  
PI Alen P;  
XX  
PI WPI; 2003-268322/26.  
XX  
XX  
PT Determining a toxicological response to an agent, useful for screening of  
PT drugs, comprises comparing the expression profile of one or more human  
PT toxic response genes to a reference gene expression profile indicative of  
PT toxicity.  
XX  
PS Claim 1; Page 271; 455pp; English.  
XX  
XX The present invention describes a method (M1) for determining a  
XX toxicological response to an agent, which comprises comparing the  
XX expression profile of one or more human toxic response genes to a  
XX reference gene expression profile indicative of toxicity, and so  
XX determining the presence of a toxic response to the agent. Also  
XX described: (1) an array comprising one or more polynucleotides selected  
XX from the genes corresponding to the partial sequences given in AB282842  
XX to AB284764, or their fragments of at least 20 nucleotides, or homologues  
XX; and (2) determining if a gene putatively identified to be a toxic  
XX response gene plays a role on toxic response pathways by determining the  
XX expression profile of the gene after exposure of cells or a human subject  
XX to a known toxic pharmaceutical or industrial agent, comprising: (a)  
XX exposing cells to an agent or isolating cells from a human subject who  
XX was exposed to an agent; (b) obtaining the test gene expression profile  
XX for a putatively identified toxic response gene after exposure to a known  
XX toxic pharmaceutical or industrial agent; and (c) comparing the test  
XX profile to the expression profile of a gene with a similar function or  
XX comparing the test profile to the expression profile of that gene after  
XX exposure to other known toxic compounds. The methods are useful for  
XX predicting and determining toxicological responses on a cellular, organ  
XX or system level. The arrays comprising the human genes are useful for  
XX toxicological screening of drugs, pharmaceutical compounds and chemicals  
XX  
SQ Sequence 1024 BP; 287 A; 197 C; 260 G; 280 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 25; DB 10; Length 1024;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25  
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227  
XX  
RESULT 15  
AA062614/c  
ID AA062614 standard; DNA; 1318 BP.  
XX  
AC AA062614;  
XX  
XX 25-MAR-2003 (revised)  
XX  
DE 17-JAN-1995 (first entry)  
XX  
DE Human mdr-1 promoter fragment.  
XX  
KW inducible promoter; cytosine agent; adriamycin; vincristine;  
KW multiple drug resistance; mdr-1; mammalian expression vector;  
KW cancer therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN DE4238778-A1.

XX 19-MAY-1994.  
 PD 12-NOV-1992; 92DE-04238778.  
 XX 12-NOV-1992; 92DE-04238778.  
 PE 12-NOV-1992; 92DE-04238778.  
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
 PA Stein U, Walther W;  
 XX WPI; 1994-168680/21.  
 DR  
 XX New mammalian expression vector useful for gene therapy, - comprising the  
 PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to  
 PT cytosstatic agents.  
 XX  
 PS Claim 2; Page 5; 7pp; German.  
 XX  
 CC This is a preferred fragment of the mdr-1 gene promoter, isolated from  
 CC human DNA. The mdr-1 promoter and enhancer elements are inducible by  
 CC cytosstatic agents such as vincristine and adriamycin which are used in  
 CC cancer therapy. Vectors comprising the promoter and enhancer sequences  
 CC operably linked to heterologous genes coding for therapeutic agents are  
 CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,  
 CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the  
 CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 CC  
 SQ Sequence 1318 BP; 430 A; 237 C; 277 G; 374 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 1318;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGCTCAGCCGACCCCGGCGCTG 25  
 ||||||||||||||||||||  
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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	582	BP218711	BP218711
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4	20.2	80.8	634	CD737438	CD737438
5	20.2	80.8	652	BU382879	BU382879
6	20.2	80.8	738	BU122038	BU122038
7	20.2	80.8	816	BU287542	BU287542
8	20.2	80.8	929	BU376890	BU376890
9	20.2	80.8	1000	BU845700	BU845700
10	20.2	80.8	1017	BU219968	BU219968
11	20.2	80.8	1440	BC015458	BC015458
12	19.2	76.8	319	AM554719	AM554719
13	19.2	76.8	401	AV653420	AV653420
14	19.2	76.8	452	AV589422	AV589422
15	19.2	76.8	485	CR846580	CR846580
16	19.2	76.8	486	BM445737	BM445737
17	19.2	76.8	488	BT726148	BT726148
18	19.2	76.8	514	BM431190	BM431190
19	19.2	76.8	532	CB423537	CB423537
20	19.2	76.8	535	BE212025	BE212025
21	19.2	76.8	536	BF046010	BF046010
22	19.2	76.8	553	BX259366	BX259366
23	19.2	76.8	558	BO819612	BO819612
24	19.2	76.8	574	BE725747	BE725747

25	19.2	76.8	578	2	BF040164	BF040164
26	19.2	76.8	593	4	BI527608	BI527608
27	19.2	76.8	601	7	CO885514	CO885514
28	19.2	76.8	623	5	BO809798	BO809798
29	19.2	76.8	632	2	BF045698	BF045698
30	19.2	76.8	633	2	BM003827	BM003827
31	19.2	76.8	652	4	BG855426	BG855426
32	19.2	76.8	652	4	BG857646	BG857646
33	19.2	76.8	665	4	BI720235	BI720235
34	19.2	76.8	670	5	BO808123	BO808123
35	19.2	76.8	681	7	CK847926	CK847926
36	19.2	76.8	692	4	BG845541	BG845541
37	19.2	76.8	733	5	BX107320	BX107320
38	19.2	76.8	737	7	CO887857	CO887857
39	18.8	75.2	406	4	BG904765	BG904765
40	18.8	75.2	443	6	CA692236	CA692236
41	18.8	75.2	622	1	AL677976	AL677976
42	18.8	75.2	641	1	AL960041	AL960041
43	18.8	75.2	649	1	AL846843	AL846843
44	18.8	75.2	687	6	CD874424	CD874424
45	18.8	75.2	737	7	CN165319	CN165319

## ALIGNMENTS

RESULT 1  
BP218711/c  
LOCUS  
DEFINITION BP218711 Sugano cDNA library, caudate nucleus Homo sapiens CDNA  
clone CNR05381, mRNA sequence.  
ACCESSION BP218711  
VERSION BP218711.1 GI:52091614  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 582)  
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,  
Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
Genome Res. 14 (9), 1711-1718 (2004)  
JOURNAL  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yensuzuki@ims.u-tokyo.ac.jp.  
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/clone="CNR05381"  
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Query Match 100.0%; Score 25; DB 5; Length 582;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GTGCTACGCCACCGCCCGGCGCTG 25  
Db 472 GTGCTACGCCACCGCCCGGCGCTG 448  
RESULT 2  
LOCUS BP348942/c  
DEFINITION BP348942 Sugano cDNA library, brain Homo sapiens CDNA clone  
SZR02494, mRNA sequence.  
582 bp mRNA linear EST 17-SEP-2004

accession BP348942 GI:52278927  
 version EST.  
 keywords Homo sapiens (human)  
 source Homo sapiens  
 organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 reference 1 (bases 1 to 582)  
 authors Suzuki,Y., Yamashita,R., Hirota,M., Sakakibara,Y., Chiba,J.,  
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
 title Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 journal Genome Res. 14 (9), 1711-1718 (2004)  
 comment Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
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 /clone\_lib="Sugano cDNA library, brain"  
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 Oy 1 GTGCTCAGCCCAAGCCCGCGCGCTG 25  
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 Db 382 GTGCTCAGCCCAAGCCCGCGCGCTG 358  
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 RESULT 3  
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 LOCUS  
 DEFINITION  
 BB608269 RIKEN full-length enriched, 2 days pregnant adult female  
 oviduct Mus musculus cDNA clone E230010P14 5', mRNA sequence.  
 accession BB608269  
 version  
 keywords  
 BB608269.1 GI:1156346  
 EST.  
 source  
 Mus musculus (house mouse)  
 organism Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 280)  
 authors  
 reference  
 1 (bases 1 to 280)  
 title  
 journal  
 comment  
 Email: genome-res@gsfc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagao,K.,  
 Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 The mouse genome project: a resource for biological, medical and  
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 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Saitama-shi, Saitama, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsfc.riken.jp, URL: http://genome.gsc.riken.jp/  
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 1-7-22 Saitama-shi, Saitama

treatalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Tsch.M., Kitzmann,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers

1..280

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="E23010P14"

/sex="female"

/tissue\_type="oviduct"

/dev\_stage="2 days pregnant adult"

/lab\_host="MDH10B"

/clone\_lib="RIKEN full-length enriched, 2 days pregnant adult female oviduct"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'

GAGGAGAAGACGGCGCCCACTCGAGTTTGTTCCTTTTTCVN 3'] cDNA was prepared by using treatalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAGGAGAAGATTCGAGTTATTATTATTATCCTCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I."

ORIGIN

Query Match 80.8%; Score 20.2; DB 2; Length 280;  
Best Local Similarity 88.0%; Pred. No. 1.6e+03;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCGCGCGCGCTG 25 -  
          |||||

DB 95 GTGCTCAGCGCGCGCCCAAGCGCTG 71  
          |||||

RESULT 4  
CD737438/c

LOCUS CD737438 634 bp mRNA linear EST 26-JUN-2003

DEFINITION 40222525 IGAL - Chicken Intestinal Lymphocyte Gallus gallus cDNA

ACCESSION clone IGAL\_80L46 5', mRNA sequence.  
CD737438

VERSION CD737438.1 GI:32286287

KEYWORDS EST.

SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Eucelostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianidae; Gallus.

REFERENCE 1 (bases 1 to 634)  
Min,W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van Raesele,C. and Han,J.Y.

AUTHORS Chicken intestinal lymphocyte EST database as a resource for the analysis of mucosal immune function  
Unpublished (2003)

JOURNAL Contact: Hyun S. Lillehoj  
Animal Parasite Diseases Laboratory  
Animal and Natural Resources Institute, USDA  
Bldg. 1043, BARC-East, Beltsville, MD 20705, USA

FEATURES  
source  
Tel: 3015048771  
Fax: 3015045103  
Email: h1111eh@anrl.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt '' -trim fasta. Vector identified  
by cross match using options -mismatch 12 -mismatch 18  
Plate: 80 row: L column: 16  
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High quality sequence stop: 634.  
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infected with coccidia duodenum and middle gut."

## ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 634;  
Best Local Similarity 88.0%; Pred. No. 1.4e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCTAGCCCGCCCGCGCGCTG 25  
|||  
557 GTACTCAGCCCGCCCTCAGCGCTG 533

RESULT 5  
BU382879/c 652 bp mRNA linear EST 28-NOV-2002  
LOCUS 60358284FP1 CSEQCHN75 Gallus gallus cDNA clone CHEST534a14 5', mRNA  
DEFINITION  
sequence.  
ACCESSION BU382879  
VERSION BU382879.1 GI:25890880  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 652)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken CDNA  
Curr. Biol. 12 (22), 1965-1969 (2002)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

Location/Qualifiers  
1. 652  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="white leghorn, Hixex"  
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/dev\_stage="3c"  
/lab\_host="DH10B"

/clone\_1lb="CSEQCHN75"  
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Site 1: EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunt-ended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
1994 91: 9228-9232 and Bonaldo et al., Genome Research 6  
1996 6: 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 652;  
Best Local Similarity 88.0%; Pred. No. 1.4e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCTAGCCCGCCCGCGCGCTG 25  
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562 GTACTCAGCCCGCCCTCAGCGCTG 538

RESULT 6  
BU122038/c 738 bp mRNA linear EST 25-NOV-2002  
LOCUS 603147071F1 CSEQCHL17 Gallus gallus cDNA clone CHEST147n17 5', mRNA  
DEFINITION  
sequence.  
ACCESSION BU122038  
VERSION BU122038.1 GI:25332165  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 738)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken CDNA  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

Location/Qualifiers  
1. 738  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST147n17"  
/sex="female"  
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/lab\_host="DH10B"  
/clone\_1lb="CSEQCHL17"  
/note="Organ: kidney + adrenal; Vector: pBluescript II  
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uni-directionally cloned cDNA libraries from messenger RNA  
for improved 3' end DNA sequencing by Glenn Fu, et al.  
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with  
NotI and EcoRI. Ligate in double stranded adaptor

containing Bsg1 and BamH1 sites  
[5'ggcgcgcgcagcccgatccgaataaaag]  
[5'aatctcttttcggatccggcgatgcgcgc]

## ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 738;  
Best Local Similarity 88.0%; Pred. No. 1.4e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCGACCGCCGCGCTG 25  
|||  
Db 561 GTACTCAGCCGACCGCTCAGCGCTG 537

RESULT 7  
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LOCUS  
DEFINITION 816 bp mRNA linear EST 27-NOV-2002  
603608037P1 CSEQCHN55 Gallus gallus CDNA clone CHEST593110 5', mRNA  
sequence.

ACCESSION BU287542  
VERSION BU287542.1 GI:25736998  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
AUTHORS Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken CDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392

## COMMENT

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

## FEATURES

source

1..816  
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/lab\_host="DH10B"  
/clone\_lib="CSEQCHN55"  
/note="Organ: kidney + adrenal; Vector: pBluescript II  
KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized  
library was constructed from 1 million independent clones.  
cDNA synthesis was initiated using an oligo(dT) primer,  
using methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was bluntended, ligated to NotI adapters, digested with  
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compatible sites of a custom modified MCS of the  
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rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 816;  
Best Local Similarity 88.0%; Pred. No. 1.4e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCGACCGCCGCGCTG 25  
|||  
Db 572 GTACTCAGCCGACCGCTCAGCGCTG 548

RESULT 8  
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LOCUS  
DEFINITION 929 bp mRNA linear EST 28-NOV-2002  
603812819P1 CSEQCHN74 Gallus gallus CDNA clone CHEST80265 5', mRNA  
sequence.

ACCESSION BU376890  
VERSION BU376890.1 GI:25884891  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
AUTHORS Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken CDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
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Location/Qualifiers

## FEATURES

source

1..929  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST80265"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN74"  
/note="Organ: kidney + adrenal; Vector: pBluescript II  
KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized  
library was constructed from 1 million independent clones.  
cDNA synthesis was initiated using an oligo(dT) primer,  
using methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was bluntended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 929;  
Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCGACCGCCGCGCTG 25  
|||  
Db 63 GTACTCAGCCGACCGCTCAGCGCTG 39

RESULT 9  
BU845700  
LOCUS  
DEFINITION 1000 bp mRNA linear EST 16-OCT-2002  
AGENCOURT\_10414348 NIH\_MGC\_109 Homo sapiens CDNA clone



IMAGE:6579377 5', mRNA sequence.  
 ACCESSION B0845700  
 VERSION B0845700.1 GI:24030141  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1000)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: L1CM2782 row: 3 column: 17  
 High quality sequence start: 14  
 High quality sequence stop: 443.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6579377"  
 /tissue\_type="teratocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_109"  
 /note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 80.8%; Score 20.2; DB 5; Length 1000;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 1 GTGCTCAGCCAGCGCCCGGCGCTG 25  
 Db 28 GGCGCTGTGCCCCCGCGCGCTG 52

RESULT 10  
 B0219968  
 LOCUS B0219968 1017 bp mRNA linear EST 02-MAY-2002  
 DEFINITION AGENCOURT 7594073 NIH\_MGC\_70 Homo sapiens CDNA clone IMAGE:6021580  
 5', mRNA sequence.  
 ACCESSION B0219968  
 VERSION B0219968.1 GI:20401357  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1017)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: L1AM13227 row: 1 column: 05  
 High quality sequence stop: 425.  
 Location/Qualifiers  
 1..1017  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6021580"  
 /tissue\_type="epithelioid carcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_70"  
 /note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."

ORIGIN  
 Query Match 80.8%; Score 20.2; DB 5; Length 1017;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 1 GTGCTCAGCCAGCGCCCGGCGCTG 25  
 Db 84 GGCGCTGTGCCCCCGCGCGCTG 108

RESULT 11  
 B015458/c  
 LOCUS B015458 1440 bp mRNA linear HTC 04-MAR-2003  
 DEFINITION Homo sapiens, clone IMAGE:3456552, mRNA.  
 ACCESSION B015458  
 VERSION B015458.1 GI:21955332  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1440)  
 AUTHORS Strauberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-7590, USA  
 COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov  
 Contact: MGC help desk  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: http://www.sngc.stanford.edu  
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Series: IRAP Plate: 4 Row: 1 Column: 17  
 This clone has the following problem: retained intron.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3456552"  
 /tissue\_type="Cervix, carcinoma"  
 /clone\_id="NIH\_MGC\_12"

ORIGIN /lab host="DH10B"  
/note="Vector: pCMV-SPORT6"

Query Match 80.8%; Score 20.2; DB 3; Length 1440;  
Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCGCGCGGCTG 25  
Db 210 GGCTCTGCCCCCGCGGCGCTG 186

RESULT 12  
LOCUS AM354719 319 bp mRNA linear EST 25-APR-2001  
DEFINITION 36851 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.  
ACCESSION AM354719  
VERSION AM354719.1 GI:6853709  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Smith,T.P.L., Grosse,W.M., Preking,B.A., Roberts,A.J., Stone,R.T.,  
Cassas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C.,  
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,  
Chitko-Mckom,C.G., Pettes,G., Holt,I., Karanycheva,S., Liang,F.,  
Quackenbush,J. and Keefe,J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle

TITLE  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
PUBMED 11282978

COMMENT

Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smitt@email.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.960904.e. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options.  
PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 9 row: M column: 16  
Seq primer: TAATACGACTCACTATGAGG.  
Location/Qualifiers

FEATURES  
source 1..319

/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 4BOV"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
library made from pooled tissue from day 20 and day 40  
embryos."

ORIGIN

Query Match 76.8%; Score 19.2; DB 2; Length 319;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTAGCCCGCGCGGCTG 25  
Db 313 TGCTAGCCCGCGGCTG 290

RESULT 13

AV663420/c 401 bp mRNA linear EST 28-NOV-2001  
LOCUS AV663420 Bos taurus brain fetus Bos taurus cDNA clone E1BR036E05  
DEFINITION 3', mRNA sequence.

ACCESSION AV663420  
VERSION AV663420.1 GI:9922450  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.  
1 (bases 1 to 401)  
Establishment of a high throughput EST sequencing system using  
poly(A) tail-removed cDNA libraries and determination of 36,000  
bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)  
MEDLINE 21570554  
PUBMED 11713328

COMMENT Contact: Yoshikazu Sugimoto  
Animal Genetics Division  
Shirakawa Institute of Animal Genetics  
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan  
Tel: 81-248-25-5641  
Fax: 81-248-25-5725  
Email: kazusugi@cocoa.ocn.ne.jp  
Single pass sequencing.  
This clone was obtained from a polyA-deleted cDNA library.  
Location/Qualifiers

FEATURES  
source 1..401

/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone\_lib="E1BR036E05"  
/tissue\_type="brain"  
/dev\_stage="fetus"  
/lab\_host="DH10B"  
/clone\_lib="Bos taurus brain fetus"  
/note="Vector: pZ1, Site 1: SalI; Site 2: NotI; Poly A  
was deleted from a NotI site"

ORIGIN

Query Match 76.8%; Score 19.2; DB 1; Length 401;  
Best Local Similarity 87.5%; Pred. No. 3.6e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTAGCCCGCGCGGCTG 25  
Db 284 TGCTAGCCCGCGGCTG 261

RESULT 14

AV589422 452 bp mRNA linear EST 27-NOV-2001  
LOCUS AV589422 Bos taurus brain fetus Bos taurus cDNA clone E1BR006D03  
DEFINITION 3', mRNA sequence.

ACCESSION AV589422  
VERSION AV589422.1 GI:9700415  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.  
1 (bases 1 to 452)  
Establishment of a high throughput EST sequencing system using  
poly(A) tail-removed cDNA libraries and determination of 36,000  
bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)

MEDLINE  
PUBMED  
COMMENT

21570554  
11713328  
Contact: Yoshihazu Sugimoto  
Animal Genetics Division  
Shirakawa Institute of Animal Genetics  
Oakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan  
Tel: 81-248-25-5641  
Fax: 81-248-25-5725  
Email: kazueugi@cocoa.ocn.ne.jp

Single pass sequencing.  
This clone was obtained from a polyA-deleted cDNA library.

# FEATURES

source

location/Qualifiers  
1..452  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="E1BR006D03"  
/issue\_type="brain"  
/dev\_stage="fetus"  
/lab\_host="DH10B"  
/clone\_1lb="Bos taurus brain fetus"  
/note="Vector: pZL1; Site\_1: SalI; Site\_2: NotI; Poly A  
was deleted from a NotI site"

# ORIGIN

Query Match 76.8%; Score 19.2; DB 1; Length 452;  
Best Local Similarity 87.5%; Pred. No. 3.5e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTACGCCACGCCCGCGCTG 25  
|||||

Db 284 TGCTACGCCCTGCGCTGCGCTG 261  
|||||

# RESULT 15

CK846580/c 485 bp mRNA linear EST 05-MAR-2004  
LOCUS 969088 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.  
DEFINITION CK846580  
ACCESSION CK846580.1 GI:45207234  
VERSION EST.  
KEYWORDS Bos taurus (cow)  
SOURCE Bos taurus  
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 485)  
AUTHORS Smith,T.P.L., Groose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Cassab,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,  
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,  
Chicko-McKown,C.G., Perera,G., Holt,I., Karaymcheva,S., Liang,F.,  
Quackenbush,J. and Keefe,J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Smith TP  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross\_match v0.990329.  
Place: 74 row: H column: 8  
Seq primer: GTAATACGACTCCTATAGCG.  
Location/Qualifiers

# FEATURES

source

1..485  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"

# ORIGIN

Query Match 76.8%; Score 19.2; DB 7; Length 485;  
Best Local Similarity 87.5%; Pred. No. 3.5e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTACGCCACGCCCGCGCTG 25  
|||||

Db 315 TGCTACGCCCTGCGCTGCGCTG 292  
|||||

Search completed: February 9, 2005, 21:55:34  
Job time : 2452.85 secs

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/lab\_host="DH10B"  
/clone\_1lb="MARC 4BOV"  
/note="Vector: PCMV SPORTS; Site\_1: NotI; Site\_2: SalI;  
Library made from pooled tissue from day 20 and day 40  
embryos."

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-11  
Perfect score: 1 ccagcatctccacgaagcagatt 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenBank1:  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_on:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_by:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504308 Sequence
2	25	100.0	25	6	AX504325 Sequence
3	25	100.0	976	9	HUMMDR1A02
4	25	100.0	976	11	G19985
5	25	100.0	1022	6	AX597862
6	25	100.0	2932	6	CQ806551
7	25	100.0	2932	6	AX457064
8	25	100.0	2932	6	AX598697
9	25	100.0	2932	6	AX767353
10	25	100.0	2932	6	AX795658
11	25	100.0	2932	6	AX822109
12	25	100.0	2932	6	AX825749
13	25	100.0	2932	6	HSMDR1A
14	25	100.0	177380	6	AX706985
15	25	100.0	177380	6	AX707915
16	25	100.0	177380	5	AC002457
17	19.8	79.2	182128	5	AC147446
18	19.8	79.2	242082	2	AC121699
19	19.8	79.2	261608	2	AC097158

20	19.8	79.2	272301	2	AC133673	AC133673 Rattus no
21	19.8	79.2	349926	1	BX571660	BX571660 Mollusca
22	19.2	76.8	59032	10	BX005046	BX005046 Mouse DNA
23	19.2	76.8	67699	8	AB016815	Continuation (9 of
24	19.2	76.8	96335	10	AC073297	AC073297 Mus muscu
25	19.2	76.8	121813	2	AC147587	AC147587 Ornithoth
26	19.2	76.8	129814	9	AC116614	AC116614 Homo sapi
27	19.2	76.8	130460	5	AC098806	AC098806 Takifugu
28	19.2	76.8	148619	2	AC151162	AC151162 Bos tauru
29	19.2	76.8	151750	9	AC003665	AC003665 Homo sapi
30	19.2	76.8	16194	2	AC139647	AC139647 Rattus no
31	19.2	76.8	179880	4	AC150482	AC150482 Bos tauru
32	19.2	76.8	181004	9	CNS01DIT	AL133990 Human chr
33	19.2	76.8	189238	2	AC151176	AC151176 Bos tauru
34	19.2	76.8	194313	5	BX333807	BX333807 Zebrafish
35	19.2	76.8	198478	2	AC117692	AC117692 Mus muscu
36	19.2	76.8	203839	2	AC091288	AC091288 Mus muscu
37	19.2	76.8	207584	2	AC103892	AC103892 Rattus no
38	19.2	76.8	216892	2	AC123206	AC123206 Rattus no
39	19.2	76.8	221430	2	AC098629	AC098629 Rattus no
40	19.2	76.8	220661	2	AC132770	AC132770 Rattus no
41	19.2	76.8	240053	2	AC113002	AL113002 Mus muscu
42	19.2	76.8	250495	10	AL844873	AL844873 Mouse DNA
43	19.2	76.8	260600	2	AC115307	AC115307 Rattus no
44	19.2	76.8	300350	1	AP006574	AP006574 Gloeobact
45	19.2	76.8	346542	2	AC120727	AC120727 Rattus no

## ALIGNMENTS

RESULT 1	AX504308	Sequence 11 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504308					
DEFINITION	Sequence 11 from Patent WO0234291.					
ACCESSION	AX504308					
VERSION	AX504308.1	GI:23386126				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	1	Colgan, S.P.				
TITLE	Compositions and methods for treating hematologic malignancies and					
JOURNAL	Multiple drug resistance					
FEATURES	Patent: WO 0234291-A 11 02-MAY-2002;					
ORIGIN	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)					
source	location/Qualifiers					
	1..25					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
Query Match	100.0%;	Score 25;	DB 6;	Length 25;		
Best Local Similarity	100.0%;	Pred. No. 0.67;				
Matches	25;	Conservative	0;	Mismatches	0;	Indels
QY	1	CCAGCATCTCCACGAAGCAGATT	25			
Db	1	CCAGCATCTCCACGAAGCAGATT	25			
RESULT 2	AX504325/c	Sequence 28 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504325					
DEFINITION	Sequence 28 from Patent WO0234291.					
ACCESSION	AX504325					
VERSION	AX504325.1	GI:23386137				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1  
Colgan, S.P.  
Compositions and methods for treating hematologic malignancies and  
multiple drug resistance  
Patent: WO 0234291-A 28 02-MAY-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)  
Location/Qualifiers  
1. 25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCAGCATCTCCAGAGGAGGAGTT 25  
25 CCAGCATCTCCAGAGGAGGAGTT 1

Db 25 CCAGCATCTCCAGAGGAGGAGTT 1

RESULT 3  
HUMMDR1A02/c 976 bp DNA linear PRI 08-JAN-1995

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM

HUMMDR1A02 976 bp DNA linear PRI 08-JAN-1995  
Human P-glycoprotein (MDR1) gene, 5' flank.  
M29423.1 J05168 M18754  
M29423.1 GI:187472  
P-glycoprotein; multidrug resistance.  
2 of 26  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 976)  
Ueda, K., Pastan, I. and Gottesman, M.M.  
Isolation and sequence of the promoter region of the human  
multidrug-resistance (P-glycoprotein) gene  
J. Biol. Chem. 262 (36), 17432-17436 (1987)  
2891692  
2 (bases 1 to 976)  
Chen, C.J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and  
Rininson, I.B.  
Genomic organization of the human multidrug resistance (MDR1) gene  
and origin of P-glycoproteins  
J. Biol. Chem. 265 (1), 506-514 (1990)  
90094448  
1867175  
1967175

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Original source text: Human multidrug resistant cell line KB-V1  
DNA.  
[2] revises [1].  
Draft entry and computer-readable sequence for [1] kindly submitted  
by I.B.Rininson, 27-OCT-1989.  
Location/Qualifiers  
1. 976  
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/map="7q21"

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/note="PGY1 mRNA and intron (alt.); G00-120-712"  
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/gene="PGY1"  
/note="PGY1, intron A"  
prim\_transcript 435..>976  
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/note="PGY1 mRNA and intron (alt.)"  
569..>976  
/gene="PGY1"

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Oy 1 CCAGCATCTCCAGAGGAGGAGTT 25  
947 CCAGCATCTCCAGAGGAGGAGTT 923

Db 947 CCAGCATCTCCAGAGGAGGAGTT 923

RESULT 4  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

G19985 976 bp DNA linear STS 28-SEP-1998  
SWS10 Eric D. Green Homo sapiens STS genomic, sequence tagged  
site.  
G19985  
G19985.1 GI:1254684  
STS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 976)  
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F.,  
Weitztraub, L.A., Mohr, T.J., R.M., Peluso, D.C., Fulton, R.S.,  
Leckie, M.P. and Green, E.D.  
A collection of 1814 human chromosome 7-specific STS  
Genome Res. 7 (1), 59-64 (1997)  
97189344  
9037602  
2 (bases 1 to 976)  
Green, E.D.  
Human chromosome 7 STSs (1997)  
Unpublished (1997)  
Synonyms: PGY1  
GDB: GDB:583426  
GDB: DSRG: PGY1  
Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Primer A: AACGAGACCAAGACATTC  
Primer B: AGGCTCTCTGTGGCAAGAG  
STS size: 180  
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)  
Denaturation: 92 degrees C for 1.00 minute(s)  
Annealing: 68 degrees C for 2.00 minute(s)  
Polymerization: 72 degrees C for 2.00 minute(s)  
PCR Cycles: 35  
Thermal Cycler: PerkinElmer TC

Protocol:  
Template: 30-100 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 5 uL

Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

This STS was developed from sequence determined by another  
investigator. See GenBank record: M29423 For additional  
information about the NHGRI chromosome 7 mapping project, see  
http://www.nhgri.nih.gov/DIR/CHR/CHR7. Also see Genomics

11:548-64 (1991) [MUID=92128937].  
FEATURES  
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1. .976  
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253. .272  
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complement(413. .432)  
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Best Local Similarity 100.0%; Pred. No. 0.61;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCAGAGGACAGATT 25  
Db 947 CCAGCATCTCCAGAGGACAGATT 923  
RESULT 5  
AX597862 1022 bp DNA linear PAT 14-FEB-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
1  
Brower, M.A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arxuda  
Indig, M., Kurensky, D., Luedtke, C., Lukowski, A.A., Lyamichev, V.,  
Nett, B.P., Retner, N.D., Roever, R.T., Skrzypczynski, Z., Ziarno, W.A.,  
Comerford, J., Stump, S. and Viegut, D.D.  
Systems and method for detection assay production and sale  
Patent: WO 0244994-A 136 06-JUN-2002;  
THIRD WAVE TECHNOLOGIES, INC. (US)  
FEATURES  
source  
Location/Qualifiers  
1. .1022  
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/mol\_type="unassigned DNA"  
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Best Local Similarity 100.0%; Pred. No. 0.61;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCAGAGGACAGATT 25  
Db 806 CCAGCATCTCCAGAGGACAGATT 830  
RESULT 6  
CQ806551 2932 bp DNA linear PAT 10-MAY-2004  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1

AUTHORS  
Roekens, J., Harbeck, N., Koenig, T., Maier, S., Martens, J., Model, F.,  
Mimmerich, I., Rujan, T., Schmitt, A., Schmitt, M., Look, M.P. and  
Marx, A.  
Method and nucleic acids for the improved treatment of breast cell  
proliferative disorders  
Patent: WO 2004035803-A 1 29-APR-2004;  
EpiGenomics AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1. .2932  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCAGAGGACAGATT 25  
Db 1594 CCAGCATCTCCAGAGGACAGATT 1570  
RESULT 7  
AX457064 2932 bp DNA linear PAT 06-JUL-2002  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
1  
Berlin, K.  
Method for the detection of cytosine methylations  
Patent: WO 0231186-A 25 18-APR-2002;  
EpiGenomics AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1. .2932  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.59;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCAGAGGACAGATT 25  
Db 1594 CCAGCATCTCCAGAGGACAGATT 1570  
RESULT 8  
AX598697 2932 bp DNA linear PAT 14-FEB-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
1  
Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,  
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Leech, R., Leu, E.,  
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,  
Pelet, C. and Ziebarth, H.  
Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders

JOURNAL Patent: WO 0207272-A 37 03-OCT-2002;  
EpiGenomics AG (DE)  
FEATURES Location/Qualifiers  
SOURCE 1..2932  
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QY 1 CCAGCATCTCCAGAGCAGAGTT 25  
DB 1594 CCAGCATCTCCAGAGCAGAGTT 1570

RESULT 9  
AX767353/c 2932 bp DNA linear PAT 02-JUL-2003  
LOCUS Sequence 1 from Patent WO03044226.  
DEFINITION AX767353  
ACCESSION AX767353  
VERSION AX767353.1 GI:32435958  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and Nimmrich,I.  
TITLE Method and nucleic acids for the analysis of a lymphoid cell proliferative disorder  
JOURNAL Patent: WO 03044226-A 1 30-MAY-2003;  
EpiGenomics AG (DE)  
FEATURES Location/Qualifiers  
SOURCE 1..2932  
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Best Local Similarity 100.0%; Pred. No. 0.59;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGCAGAGTT 25  
DB 1594 CCAGCATCTCCAGAGCAGAGTT 1570

RESULT 10  
AX795658/c 2932 bp DNA linear PAT 04-OCT-2003  
LOCUS Sequence 1 from Patent WO03052135.  
DEFINITION AX795658  
ACCESSION AX795658  
VERSION AX795658.1 GI:37516324  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S. and Nimmrich,I.  
TITLE Method and nucleic acids for the analysis of a lung cell proliferative disorder  
JOURNAL Patent: WO 03052135-A 1 26-JUN-2003;  
EpiGenomics AG (DE)  
FEATURES Location/Qualifiers  
SOURCE 1..2932  
/organism="Homo sapiens"

JOURNAL Patent: WO 0207272-A 37 03-OCT-2002;  
EpiGenomics AG (DE)  
FEATURES Location/Qualifiers  
SOURCE 1..2932  
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ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 2932;  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGCAGAGTT 25  
DB 1594 CCAGCATCTCCAGAGCAGAGTT 1570

RESULT 11  
AX822109/c 2932 bp DNA linear PAT 11-DEC-2003  
LOCUS Sequence 1 from Patent EP1340818.  
DEFINITION AX822109  
ACCESSION AX822109  
VERSION AX822109.1 GI:39748737  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R., Rujan,T. and Schmitt,A.  
TITLE Method and nucleic acids for the analysis of a colon cell proliferative disorder  
JOURNAL Patent: EP 1340818-A 1 03-SEP-2003;  
EpiGenomics AG (DE)  
FEATURES Location/Qualifiers  
SOURCE 1..2932  
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QY 1 CCAGCATCTCCAGAGCAGAGTT 25  
DB 1594 CCAGCATCTCCAGAGCAGAGTT 1570

RESULT 12  
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LOCUS Sequence 1 from Patent WO03072821.  
DEFINITION AX825749  
ACCESSION AX825749  
VERSION AX825749.1 GI:39751263  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R., Rujan,T. and Schmitt,A.  
TITLE Method and nucleic acids for the analysis of a colon cell proliferative disorder  
JOURNAL Patent: WO 03072821-A 1 04-SEP-2003;  
EpiGenomics AG (DE)  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 2932;



Best Local Similarity 100.0%; Pred. No. 0.59; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1594 CCAGCATCTCCAGCAGCAGAGTT 1570

RESULT 13  
HSMRIA/c 2932 bp DNA linear PRI 05-NOV-1997

DEFINITION Human MDR1 (multidrug resistance) gene for P-glycoprotein.

VERSION X58723.X59732

KEYWORDS MDR1 gene; multidrug resistance glycoprotein; P-glycoprotein.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 2932)

AUTHORS Kioke,N., Yamano,Y., Komano,T., Gotteaman,M.M., Pastan,I. and Ueda,K.

TITLE P-glycoprotein gene (MDR1) cDNA from human adrenal: normal P-glycoprotein carries Gly185 with an altered pattern of multidrug resistance

JOURNAL Biochem. Res. Commun. 162 (1), 224-231 (1989)

MEDLINE 89322246

PUBMED 2568932

REFERENCE 2 (bases 1 to 2932)

AUTHORS Kioke,N., Yamano,Y., Komano,T. and Ueda,K.

TITLE Heat-shock responsive elements in the induction of the multidrug resistance gene (MDR1)

JOURNAL FEBS Lett. 301 (1), 37-40 (1992)

MEDLINE 93083619

PUBMED 1360409

REFERENCE 3 (bases 1 to 2932)

AUTHORS Kioke,N.

TITLE Direct Submision

JOURNAL Submitted (04-APR-1991) N. Kioke, Laboratory of Biochemistry, Dept of Agricultural Chemistry, Kyoto University, Kitashirikawa

COMMENT See Upn. J. Cancer Res. 80:1127-1132(1989) for overlapping sequence.

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GC\_signal 1022..1032

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exon 1772..1846  
/gene="MDR1"

number=2

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Qy 1 CCAGCATCTCCAGCAGCAGAGTT 25  
Db 1594 CCAGCATCTCCAGCAGCAGAGTT 1570

RESULT 14

LOCUS AX706985 177380 bp DNA linear PAT 04-APR-2003

DEFINITION Sequence 683 from Patent WO03013534.

ACCESSION AX706985

VERSION AX706985.1 GI:29563306

KEYWORDS Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1

AUTHORS Heinrich,G. and Kerb,R.

TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5

JOURNAL Patent: WO 03013534-A 683 20-FEB-2003;  
Epidaurus Biotechnology AG (DE)

FEATURES  
source 1..177380  
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/db\_xref="caxon:9606"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.53;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGCAGCAGAGTT 25  
Db 141346 CCAGCATCTCCAGCAGCAGAGTT 141322

RESULT 15

LOCUS AX707915 177380 bp DNA linear PAT 04-APR-2003

DEFINITION Sequence 683 from Patent WO03013536.

ACCESSION AX707915

VERSION AX707915.1 GI:29563986

KEYWORDS Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1

AUTHORS Heinrich,G. and Kerb,R.

TITLE Methods for treatment of cancer using irinotecan based on UGT1A1

JOURNAL Patent: WO 03013536-A 683 20-FEB-2003;  
Epidaurus Biotechnology AG (DE)

FEATURES  
source 1..177380  
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/mol\_type="unassigned DNA"

ORIGIN /db\_xref="taxon:9606"

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QY 1 CCAGCATCTCCACGAGGACAGATT 25  
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Search completed: February 9, 2005, 17:01:58  
 Job time : 485.178 secs



;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 189128  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-189128

Query Match 75.2%; Score 18.8; DB 4; Length 601;  
Best Local Similarity 90.9%; Pred. No. 66;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATCTCCAGGAGGCGAGATT 25  
Db 309 GCAGCTCCAGGAGGCGAGATT 330

RESULT 3  
US-09-949-016-17153/c  
; Sequence 17153, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C0001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 17153  
; LENGTH: 76401  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17153

Query Match 75.2%; Score 18.8; DB 4; Length 76401;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATCTCCAGGAGGCGAGATT 25  
Db 28802 GCAGCTCCAGGAGGCGAGATT 28781

RESULT 4  
US-09-252-991A-13079/c  
; Sequence 13079, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13079  
; LENGTH: 2028  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13079

Query Match 74.4%; Score 18.6; DB 4; Length 2028;  
Best Local Similarity 84.0%; Pred. No. 95;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGCGAGATT 25  
Db 1187 CCAGCTTGTCAGCAAGGAAGAGATT 1163

RESULT 5  
US-09-252-991A-12708  
; Sequence 12708, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 12708  
; LENGTH: 3525  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12708

Query Match 74.4%; Score 18.6; DB 4; Length 3525;  
Best Local Similarity 84.0%; Pred. No. 1e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGCGAGATT 25  
Db 1998 CCAGCTTGTCAGCAAGGAAGAGATT 2022

RESULT 6  
US-09-252-991A-13251/c  
; Sequence 13251, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13251  
; LENGTH: 3906  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13251

Query Match 74.4%; Score 18.6; DB 4; Length 3906;  
Best Local Similarity 84.0%; Pred. No. 1e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGCGAGATT 25  
Db 2218 CCAGCTTGTCAGCAAGGAAGAGATT 2194

RESULT 7

US-09-949-016-164913  
Sequence 164913, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL0001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ. ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 164913  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-164913

Query Match 72.8%; Score 18.2; DB 4; Length 601;  
Best Local Similarity 87.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGCAGAG 23  
DB 16 CCAGCACCCTCCAGAGAGCTGAG 38

RESULT 8  
US-08-615-170-20/c  
Sequence 20, Application US/08615170  
Patent No. 5776776  
GENERAL INFORMATION:  
APPLICANT: ORDAHL, Charles P.  
APPLICANT: AZAKIE, Anthony  
APPLICANT: MAR, Janet H.  
APPLICANT: FARRANCE, Iain K.G.  
APPLICANT: HALL, Deborah E.  
APPLICANT: STEWART, Alexandre F.R.  
APPLICANT: LARKIN, Sarah B.  
TITLE OF INVENTION: DREF-1 ISOFORMS AND USES THEREOF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,170  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01526  
FILING DATE: 06-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/191,493  
FILING DATE: 04-FEB-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Heslin, James W.

REGISTRATION NUMBER: 29,541  
REFERENCE/DOCKET NUMBER: 2307U-053120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1894 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-615-170-20

Query Match 72.8%; Score 18.2; DB 1; Length 1894;  
Best Local Similarity 87.0%; Pred. No. 1.4e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGAGCAGAGT 24  
DB 1054 CGGCACCTCATGAGCAGAGT 1032

RESULT 9  
US-08-615-170-18/c  
Sequence 18, Application US/08615170  
Patent No. 5776776  
GENERAL INFORMATION:  
APPLICANT: ORDAHL, Charles P.  
APPLICANT: AZAKIE, Anthony  
APPLICANT: MAR, Janet H.  
APPLICANT: FARRANCE, Iain K.G.  
APPLICANT: HALL, Deborah E.  
APPLICANT: STEWART, Alexandre F.R.  
APPLICANT: LARKIN, Sarah B.  
TITLE OF INVENTION: DREF-1 ISOFORMS AND USES THEREOF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,170  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01526  
FILING DATE: 06-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/191,493  
FILING DATE: 04-FEB-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Heslin, James W.  
REGISTRATION NUMBER: 29,541  
REFERENCE/DOCKET NUMBER: 2307U-053120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1897 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-615-170-18

Query Match 72.8%; Score 18.2; DB 1; Length 1897;  
Best Local Similarity 87.0%; Pred. No. 1.4e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGAGGAGGAGT 24  
Db 1057 CGGCACCTCCATGAGGAGGAGT 1035

RESULT 10  
US-09-949-016-4640/c  
Sequence 4640, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4640  
LENGTH: 2087  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4640

Query Match 72.8%; Score 18.2; DB 4; Length 2087;  
Best Local Similarity 87.0%; Pred. No. 1.4e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGGAGGAG 23  
Db 319 CCAGCAGCTCCAGAGGAGGAG 297

RESULT 11  
US-08-387-942C-1  
Sequence 1, Application US/08387942C  
Patent No. 5939289  
GENERAL INFORMATION:  
APPLICANT: ERTESVAG, HELGA  
APPLICANT: VALLA, SVEIN  
APPLICANT: SKJAK-BRAEK, GUDMUND  
APPLICANT: LARSEN, BJORN  
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES  
TITLE OF INVENTION: ENCODING MANNUONAN C-5-EPIMERASE  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
STREET: P.O. BOX 747  
CITY: FALIS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22042  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,942C

FILING DATE: 09-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1809-106P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8050  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1258 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: Azotobacter vinelandii  
STRAIN: E  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 290..1951  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2227..6438  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 6702..9695  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 9973..12588  
US-08-387-942C-1

Query Match 72.8%; Score 18.2; DB 2; Length 12588;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGGAGGAG 23  
Db 8771 CCAGCAGCTCTCCAGAGGAGGAG 8793

RESULT 12  
US-09-949-016-16382/c  
Sequence 16382, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16382  
LENGTH: 36103  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16382

Query Match 72.8%; Score 18.2; DB 4; Length 36103;  
Best Local Similarity 87.0%; Pred. No. 2.1e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGGAGGAG 23

Db 16613 CCAGCATCTCCAGCAAGGAGT 16591

## RESULT 13

US-09-949-016-15083  
Sequence 15083, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15083  
LENGTH: 50850  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(50850)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15083

Query Match 72.8%; Score 18.2; DB 4; Length 50850;  
Best Local Similarity 87.0%; Pred. No. 2.2e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGCAAGGAGT 24  
Db 512 CAGACTCTCCACAAAGCGAGT 534

## RESULT 14

US-09-949-016-15084  
Sequence 15084, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15084  
LENGTH: 50850  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(50850)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15084

Query Match 72.8%; Score 18.2; DB 4; Length 50850;  
Best Local Similarity 87.0%; Pred. No. 2.2e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGCAAGGAGT 24  
Db 512 CAGACTCTCCACAAAGCGAGT 534

## RESULT 15

US-09-949-016-15085  
Sequence 15085, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15085  
LENGTH: 50850  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(50850)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15085

Query Match 72.8%; Score 18.2; DB 4; Length 50850;  
Best Local Similarity 87.0%; Pred. No. 2.2e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGCAAGGAGT 24  
Db 512 CAGACTCTCCACAAAGCGAGT 534

Search completed: February 9, 2005, 17:11:16  
Job time : 80.592 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds  
(without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-11

Perfect score: 25  
1 ccagcattcccaagagcagcagc 25

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 413806 seqs, 287871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubna/PC1\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubna/PC1US\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	1021	17	US-10-321-039-24
2	25	100.0	2932	18	US-10-473-126-37
3	19.2	76.8	561	18	US-10-767-701-25185
4	19.2	76.8	619	18	US-10-425-115-59217
5	18.6	74.4	60	10	US-09-908-975-9939
6	18.6	74.4	2797	17	US-10-336-603A-7
7	18.6	74.4	2914	17	US-10-336-603A-9
8	18.6	74.4	2963	17	US-10-444-575-5
9	18.6	74.4	2963	17	US-10-440-464-125
10	18.6	74.4	2968	17	US-10-335-603A-11
11	18.6	74.4	3058	9	US-09-964-824A-234

c 12	18.6	74.4	3058	9	US-09-880-107-1654	Sequence 1654, Ap
c 13	18.6	74.4	3058	17	US-10-336-603A-5	Sequence 5, Appl
c 14	18.6	74.4	684187	18	US-10-367-094-71	Sequence 71, Appl
c 15	18.2	72.8	494	13	US-10-027-632-230104	Sequence 230104,
c 16	18.2	72.8	494	13	US-10-027-632-230104	Sequence 230104,
c 17	18.2	72.8	945	17	US-10-027-632-30739	Sequence 30739, A
c 18	18.2	72.8	945	17	US-10-027-632-30739	Sequence 30739, A
c 19	18.2	72.8	1346	9	US-09-805-020-25	Sequence 25, Appl
c 20	18.2	72.8	1422	18	US-10-437-963-75819	Sequence 75819, A
c 21	18.2	72.8	1643	9	US-09-805-020-26	Sequence 26, Appl
c 22	18.2	72.8	1717	9	US-09-805-020-24	Sequence 24, Appl
c 23	18.2	72.8	2083	17	US-10-159-563-289	Sequence 289, Ap
c 24	18.2	72.8	2196	13	US-10-087-192-1799	Sequence 1799, Ap
c 25	18.2	72.8	2345	15	US-10-101-510-504	Sequence 504, Ap
c 26	18.2	72.8	2713	9	US-09-805-020-27	Sequence 27, Appl
c 27	18.2	72.8	57013	13	US-10-087-192-1798	Sequence 1798, Ap
c 28	18	72.0	201	18	US-10-719-993-2047	Sequence 2047, Ap
c 29	18	72.0	201	18	US-10-719-993-2047	Sequence 2047, Ap
c 30	18	72.0	201	18	US-10-719-993-2047	Sequence 2047, Ap
c 31	18	72.0	2524	17	US-10-205-331-115	Sequence 115, App
c 32	18	72.0	2524	17	US-10-152-319A-2092	Sequence 2092, App
c 33	18	72.0	6519	18	US-10-719-993-109	Sequence 109, App
c 34	18	72.0	6638	18	US-10-719-993-108	Sequence 108, App
c 35	18	72.0	493999	18	US-10-719-993-6787	Sequence 6787, Ap
c 36	17.8	71.2	358	17	US-10-062-674-773	Sequence 773, App
c 37	17.8	71.2	575	11	US-09-876-143-326	Sequence 326, App
c 38	17.8	71.2	575	11	US-09-876-143-314	Sequence 314, App
c 39	17.8	71.2	1003	13	US-10-027-632-120970	Sequence 120970,
c 40	17.8	71.2	1003	13	US-10-027-632-120971	Sequence 120971,
c 41	17.8	71.2	1003	13	US-10-027-632-120972	Sequence 120972,
c 42	17.8	71.2	1003	17	US-10-027-632-120970	Sequence 120970,
c 43	17.8	71.2	1003	17	US-10-027-632-120971	Sequence 120971,
c 44	17.8	71.2	1003	17	US-10-027-632-120972	Sequence 120972,
c 45	17.8	71.2	1146	17	US-10-369-493-45219	Sequence 45219, A

# ALIGNMENTS

RESULT 1  
US-10-321-039-24  
Sequence 24, Application US/10321039  
Publication No. US20040014067A1  
GENERAL INFORMATION:  
APPLICANT: Lyamchev, Victor  
APPLICANT: Lukowlak, Andrew  
APPLICANT: Jarvis, Nancy  
APPLICANT: Kurensky, David  
TITLE OF INVENTION: Amplification Methods and Compositions  
FILE REFERENCE: FORS-06960  
CURRENT APPLICATION NUMBER: US/10/321.039  
CURRENT FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: 09/998,157  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 60/329,113  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/360,489  
NUMBER OF SEQ ID NOS: 759  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 24  
LENGTH: 1021  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (561) (561)  
OTHER INFORMATION: n can be t or c.  
US-10-321-039-24  
Query Match 100.0%; Score 25; DB 17; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGGAGGAGAGTT 25  
DB 805 CCAGCATCTCCAGGAGGAGAGTT 829

## RESULT 2

US-10-473-126-37/c  
; Sequence 37, Application US/10473126  
; Publication No. US20040234973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/473.126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 37  
; LENGTH: 2932  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-473-126-37

Query Match 100.0%; Score 25; DB 18; Length 2932;  
Best Local Similarity 100.0%; Pred. No. 0.075;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGGAGGAGAGTT 25  
DB 1594 CCAGCATCTCCAGGAGGAGAGTT 1570

## RESULT 3

US-10-767-701-25185  
; Sequence 25185, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767.701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 25185  
; LENGTH: 561  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 30948191  
US-10-767-701-25185

Query Match 76.8%; Score 19.2; DB 18; Length 561;  
Best Local Similarity 87.5%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGGAGGAGAGTT 25  
DB 382 CAGCATCTCTCCGAGGAGGAGACTT 405

## RESULT 4

US-10-425-115-59217  
; Sequence 59217, Application US/10425115  
; Publication No. US20040234272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425.115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 59217  
; LENGTH: 619  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_154001C.1  
US-10-425-115-59217

Query Match 76.8%; Score 19.2; DB 18; Length 619;  
Best Local Similarity 87.5%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGGAGGAGAGTT 25  
DB 561 CAGCATCTGCGAGGAGGAGAGTT 584

## RESULT 5

US-09-908-975-9939/c  
; Sequence 9939, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGER, Simion  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908.975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 9939  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-9939

Query Match 74.4%; Score 18.6; DB 10; Length 60;  
Best Local Similarity 84.0%; Pred. No. 76;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGGAGGAGAGTT 25  
DB 36 CCAGCACTCCGCAAGGAGGAGT 12

## RESULT 6

US-10-336-603A-7/c  
; Sequence 7, Application US/10336603A  
; Publication No. US20040072997A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-533A  
; CURRENT APPLICATION NUMBER: US/10/336.603A  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: 09/746,491  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 10/055,569  
; PRIOR FILING DATE: 2001-10-26

NUMBER OF SEQ ID NOS: 169  
SOFTWARE: CursSeqList version 0.1  
SEQ ID NO 7  
LENGTH: 2797  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (130)..(2658)  
US-10-336-603A-7

Query Match 74.4%; Score 18.6; DB 17; Length 2797;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGAGGAGCATGTT 25  
DB 1417 CCAGCTTCTCCAGAGGAGCATAGCT 1393

RESULT 7  
US-10-336-603A-9/c  
Sequence 9, Application US/10336603A  
Publication No. US20040072997A1  
GENERAL INFORMATION:  
APPLICANT: Alsbrook et al.  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-533A  
CURRENT APPLICATION NUMBER: US/10/336,603A  
CURRENT FILING DATE: 2003-01-03  
PRIOR APPLICATION NUMBER: 09/746,491  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 10/055,569  
PRIOR FILING DATE: 2001-10-26  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: CursSeqList version 0.1  
SEQ ID NO 9  
LENGTH: 2914  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (130)..(2775)  
US-10-336-603A-9

Query Match 74.4%; Score 18.6; DB 17; Length 2914;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGAGGAGCATGTT 25  
DB 1417 CCAGCTTCTCCAGAGGAGCATAGCT 1393

RESULT 8  
US-10-444-575-5/c  
Sequence 5, Application US/10444575  
Publication No. US20030232374A1  
GENERAL INFORMATION:  
APPLICANT: University of Connecticut Health Center  
APPLICANT: Kuchel, George A  
APPLICANT: Zhu, Qing  
TITLE OF INVENTION: Compositions and Methods Relating to Destrinor Estrogen-Regulated  
TITLE OF INVENTION: Protein (DEBP)  
FILE REFERENCE: UCT-0035  
CURRENT APPLICATION NUMBER: US/10/444,575  
CURRENT FILING DATE: 2003-05-22  
PRIOR APPLICATION NUMBER: US 60/382,830  
PRIOR FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5  
LENGTH: 2963

TYPE: DNA  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Tobe, T., Saguchi, K., Hashimoto, K., Miura, N.H., Tomita, M.,  
AUTHORS: Li, F., Wang, Y., Minoshima, S., and Shimizu, N.  
TITLE: Mapping of human inter-alpha-trypsin inhibitor family heavy  
TITLE: chain-related protein gene (ITIH1) to human chromosome 3p21-p14  
JOURNAL: Cytogenet. Cell Genet.  
VOLUME: 71  
ISSUE: 3  
PAGES: 296-298  
DATE: 1995  
DATABASE ACCESSION NUMBER: NM 002218  
DATABASE ENTRY DATE: 2003-04-07  
RELEVANT RESIDUES: (1)..(2963)  
US-10-444-575-5

Query Match 74.4%; Score 18.6; DB 17; Length 2963;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGAGGAGCATGTT 25  
DB 1321 CCAGCTTCTCCAGAGGAGCATAGCT 1297

RESULT 9  
US-10-440-464-125/c  
Sequence 125, Application US/10440464  
Publication No. US20040018528A1  
GENERAL INFORMATION:  
APPLICANT: DEPRIMO, SAMUEL  
APPLICANT: O'FARRELL, ANNE-MARIE  
APPLICANT: MORIMOTO, AYESA  
APPLICANT: SMOLICH, BEVERLY  
APPLICANT: MANNING, WILLIAM  
APPLICANT: WALTER, SARAH  
APPLICANT: CHERRINGTON, JULIE  
APPLICANT: SCHILLING, JIM  
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE  
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS  
FILE REFERENCE: 038602/1592  
CURRENT APPLICATION NUMBER: US/10/440,464  
CURRENT FILING DATE: 2003-05-19  
PRIOR APPLICATION NUMBER: 60/380,872  
PRIOR FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: 60/448,922  
PRIOR FILING DATE: 2003-02-24  
PRIOR APPLICATION NUMBER: 60/448,874  
PRIOR FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 185  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 125  
LENGTH: 2963  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-440-464-125

Query Match 74.4%; Score 18.6; DB 17; Length 2963;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGAGGAGCATGTT 25  
DB 1321 CCAGCTTCTCCAGAGGAGCATAGCT 1297

RESULT 10  
US-10-336-603A-11/c  
Sequence 11, Application US/10336603A  
Publication No. US20040072997A1  
GENERAL INFORMATION:  
APPLICANT: Alsbrook et al.

;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
;; FILE REFERENCE: 21402-533A  
;; CURRENT APPLICATION NUMBER: US/10/336,603A  
;; CURRENT FILING DATE: 2003-01-03  
;; PRIOR APPLICATION NUMBER: 09/746,491  
;; PRIOR FILING DATE: 2000-12-20  
;; PRIOR APPLICATION NUMBER: 10/055,569  
;; PRIOR FILING DATE: 2001-10-26  
;; NUMBER OF SEQ ID NOS: 169  
;; SOFTWARE: CuraseqList version 0.1  
;; SEQ ID NO 11  
;; LENGTH: 2968  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (130)..(2829)  
US-10-336-603A-11

Query Match 74.4%; Score 18.6; DB 17; Length 2968;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25  
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 11  
US-09-964-824A-234/c  
;; Sequence 234, Application US/09964824A  
;; Patent No. US20020102531A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Horrigan, Stephen  
;; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
;; TITLE OF INVENTION: Sets  
;; FILE REFERENCE: 669290-73  
;; CURRENT APPLICATION NUMBER: US/09/964,824A  
;; CURRENT FILING DATE: 2001-09-27  
;; PRIOR APPLICATION NUMBER: US/60/236,033  
;; PRIOR FILING DATE: 2000-09-28  
;; PRIOR APPLICATION NUMBER: US/60/236,032  
;; PRIOR FILING DATE: 2000-09-28  
;; PRIOR APPLICATION NUMBER: US/60/236,028  
;; PRIOR FILING DATE: 2000-09-28  
;; NUMBER OF SEQ ID NOS: 583  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 234  
;; LENGTH: 3058  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-964-824A-234

Query Match 74.4%; Score 18.6; DB 9; Length 3058;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25  
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 12  
US-09-880-107-1654/c  
;; Sequence 1654, Application US/09880107  
;; Patent No. US20020142981A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Horne, Darci T.  
;; APPLICANT: Vockley, Joseph G.  
;; APPLICANT: Scherf, Uwe  
;; APPLICANT: Gene Logic, Inc.  
;; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
;; FILE REFERENCE: 44921-5028-WO

;; CURRENT APPLICATION NUMBER: US/09/880,107  
;; CURRENT FILING DATE: 2001-06-14  
;; PRIOR APPLICATION NUMBER: US 60/211,379  
;; PRIOR FILING DATE: 2000-06-14  
;; PRIOR APPLICATION NUMBER: 60/237,054  
;; PRIOR FILING DATE: 2000-10-02  
;; NUMBER OF SEQ ID NOS: 3950  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1654  
;; LENGTH: 3058  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D38535  
US-09-880-107-1654

Query Match 74.4%; Score 18.6; DB 9; Length 3058;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25  
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 13  
US-10-336-603A-5/c  
;; Sequence 5, Application US/10336603A  
;; Publication No. US20040072997A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alsbjork et al.  
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
;; FILE REFERENCE: 21402-533A  
;; CURRENT APPLICATION NUMBER: US/10/336,603A  
;; CURRENT FILING DATE: 2003-01-03  
;; PRIOR APPLICATION NUMBER: 09/746,491  
;; PRIOR FILING DATE: 2000-12-20  
;; PRIOR APPLICATION NUMBER: 10/055,569  
;; PRIOR FILING DATE: 2001-10-26  
;; NUMBER OF SEQ ID NOS: 169  
;; SOFTWARE: CuraseqList version 0.1  
;; SEQ ID NO 5  
;; LENGTH: 3058  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (130)..(2919)  
US-10-336-603A-5

Query Match 74.4%; Score 18.6; DB 17; Length 3058;  
Best Local Similarity 84.0%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25  
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 14  
US-10-367-094-71  
;; Sequence 71, Application US/10367094  
;; Publication No. US20040170982A1  
;; GENERAL INFORMATION:  
;; APPLICANT: David W. Morris  
;; APPLICANT: Marc Malandro  
;; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer  
;; FILE REFERENCE: 529452001500  
;; CURRENT APPLICATION NUMBER: US/10/367,094  
;; CURRENT FILING DATE: 2003-02-14  
;; NUMBER OF SEQ ID NOS: 203  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 71

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; LENGTH: 684187
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(684187)
; OTHER INFORMATION: n = A,T,C or G
US-10-367-094-71

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Query Match          74.4%; Score 18.6; DB 18; Length 684187;
Best Local Similarity 84.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 CCAGCATCTCCACGAGCAGAGTT 25
Db      253637 CCAGCCTCTGATGATGACAGAGTT 253661

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RESULT 15
US-10-027-632-230104/c
; Sequence 230104, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230104
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-230104

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Query Match          72.8%; Score 18.2; DB 13; Length 494;
Best Local Similarity 87.0%; Pred. No. 12e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      3 AGCATCTCCACGAGCAGAGTT 25
Db      454 AGCACCCTCCACGAGCAGAGTT 432

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Job time : 268.667 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds  
(without alignments)  
602.360 Million cell updates/sec

Title: US-10-007-255-11  
Perfect score: 1  
Sequence: 1 ccagcatctccacgaagcagagct 25

Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: N\_Geneseq\_16Dec04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001as.\*
- 5: Geneseq2001bs.\*
- 6: Geneseq2002as.\*
- 7: Geneseq2002bs.\*
- 8: Geneseq2003as.\*
- 9: Geneseq2003bs.\*
- 10: Geneseq2003cs.\*
- 11: Geneseq2003ds.\*
- 12: Geneseq2004as.\*
- 13: Geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	6	AAD39000 Human mdr
2	25	100.0	25	6	AAD39010 Human mdr
3	25	100.0	2932	8	ABZ09897 Human 5'
4	25	100.0	2932	10	ADB53945 MDR1 geno
5	25	100.0	2932	10	ADB84005 5' regula
6	25	100.0	2932	13	ADS88985 Human ABC
7	25	100.0	8573	6	ABS98184 Human mdr
8	25	100.0	10200	6	AAD41243 Human MDR
9	25	100.0	177380	8	ACF62751 Cancer ba
10	25	100.0	177380	8	ADB20870 MRP1 base
11	25	100.0	177380	10	ADB87959 Human UGT
12	25	100.0	177380	10	ADB96942 Human MDR
13	25	100.0	177380	10	ADB962133 Human MDR
14	18.6	74.4	60	6	ABN37191 Human SPL
15	18.6	74.4	354	12	AD044565 A1480570e
16	18.6	74.4	807	10	ADC39482 Novel hum
17	18.6	74.4	867	10	AD09661 Novel DNA
18	18.6	74.4	1506	12	ADP28080 Human sec
19	18.6	74.4	1506	12	ADP28075 Human sec
20	18.6	74.4	2028	11	ABD14475 Pseudomon

C	21	18.6	74.4	2797	10	ADD49034
C	22	18.6	74.4	2834	12	ADJ72006
C	23	18.6	74.4	2905	12	ADJ72005
C	24	18.6	74.4	2914	10	ADD49036
C	25	18.6	74.4	2960	13	ACN37942
C	26	18.6	74.4	2963	6	AB141971
C	27	18.6	74.4	2963	12	ADH17126
C	28	18.6	74.4	2963	12	ADH19055
C	29	18.6	74.4	3058	6	ADD49038
C	30	18.6	74.4	3058	6	AB167200
C	31	18.6	74.4	3058	6	AB141972
C	32	18.6	74.4	3058	6	ABN95156
C	33	18.6	74.4	3058	10	ADD49032
C	34	18.6	74.4	3144	10	ADG75752
C	35	18.6	74.4	3489	8	ACC59960
C	36	18.6	74.4	3525	11	ABD14104
C	37	18.6	74.4	3906	11	ABD14647
C	38	18.6	74.4	4042	10	AD07449
C	39	18.6	74.4	4226	12	AD064433
C	40	18.6	74.4	5672	13	ACN42394
C	41	18.6	74.4	5763	13	ACN42392
C	42	18.6	74.4	5793	13	ACN42391
C	43	18.6	74.4	11000	13	ABD32594_2
C	44	18.6	74.4	11000	13	ABD32594_2
C	45	18.2	72.8	444	4	AA179965

# ALIGNMENTS

## RESULT 1

AAD39000 standard; DNA; 25 BP.

23-SEP-2002 (first entry)

Human mdr1-HRE antisense oligonucleotide #3.

Human; hematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma; angioendothelial metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; antisense; phosphorothioate backbone; ss.

Homo sapiens.

Synthetic.

Key	Location/Qualifiers
modified_base	1..25
/*tag= a	
/mod_base= OTHER	
/note= "phosphorothioate backbone"	

WO200234291-A2.

02-MAY-2002.

25-OCT-2001; 2001WO-US049856.

26-OCT-2000; 2000US-0243542P.

(BGM) BRIGHAM & WOMENS HOSPITAL INC.

Colgan SP;

WPI; 2002-471427/50.

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
PT binding molecules.  
XX  
PS Claim 14; Page 43; 92pp; English.  
XX  
CC The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is an antisense  
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its  
CC expression. This oligo is used in the exemplification of the invention  
XX  
SQ Sequence 25 BP; 7 A; 8 C; 6 G; 4 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCAGCATCTCCACGAGGAGGAGTT 25  
DB 1 CCAGCATCTCCACGAGGAGGAGTT 25  
  
RESULT 2  
AAD39010/C  
ID AAD39010 standard; DNA; 25 BP.  
XX  
AC AAD39010;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human mdrl gene HIF-1 binding site DNA #3.  
XX  
KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;  
KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;  
KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;  
KW angiotenic myeloid metaplasia; myeloid leukaemia; gene therapy;  
KW polycythaemia vera; hypoxia responsive element; HRE; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 11..15  
FT /\*tag= a  
FT /bound\_moiety= "HIF-1"  
XX  
PN WO200234291-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 25-OCT-2001; 2001WO-US049856.  
XX  
PR 26-OCT-2000; 2000US-0243542P.  
XX  
PA (BGM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX  
PI Colgan SP;  
XX  
DR WPI; 2002-471427/50.  
XX  
PT Treating a subject (at risk of) having a hematologic malignancy or  
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
PT binding molecules.  
XX  
PS Example 2; Page 12; 92pp; English.  
XX  
CC The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is human mdrl  
CC gene HIF-1 binding site DNA  
XX  
SQ Sequence 25 BP; 4 A; 6 C; 8 G; 7 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCAGCATCTCCACGAGGAGGAGTT 25  
DB 25 CCAGCATCTCCACGAGGAGGAGTT 1  
  
RESULT 3  
ABZ09897/C  
ID ABZ09897 standard; DNA; 2932 BP.  
XX  
AC ABZ09897;  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DE Human 5' and/or regulatory region of MDR1 DNA SEQ ID NO:37.  
XX  
KW Human; haematopoietic cell proliferation disorder; cytostatic;  
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
KW cytosine methylation state; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO20027272-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-EP003401.  
XX  
PR 26-MAR-2001; 2001US-0278333P.  
XX  
PA (EPIC-) EPICENOMICS AG.  
XX  
PI Berlin K, Braun A, Dietler J, Guertig D, Howe A, Mueller J;  
PI Oler A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;  
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
PI Schwobe I, Ziebarth H;  
XX  
DR WPI; 2003-018942/01.  
XX  
PT Detecting and differentiating between hematopoietic cell proliferative  
PT disorders, comprises contacting a target nucleic acid with a reagent that  
PT distinguishes between methylated and non-methylated CpG dinucleotides.  
XX  
PS Claim 38; SEQ ID NO 37; 117pp; English.  
XX  
CC The present invention describes a method for detecting and  
CC differentiating between haematopoietic cell proliferative disorders



associated with at least 1 gene and/or their regulatory regions in a  
CC subject. The method comprises contacting a target nucleic acid in a  
CC biological sample obtained from the subject with at least 1 reagent,  
CC which distinguishes between methylated and non-methylated CpG  
CC dinucleotides within the target nucleic acid. AB209861 to AB211118  
CC represent specifically claimed nucleotide sequences from the present  
CC invention. Oligonucleotides from the present invention can be used: for  
CC differentiating between healthy haematopoietic cells and proliferative  
CC disorder haematopoietic cells; for differentiating between acute  
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
CC determining the cytosine methylation state and/or single nucleotide  
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
CC related sequences and their complements; and as primers for the  
CC amplification of haematopoietic cell proliferation disorder related DNA  
CC sequences. The nucleotide sequences from the present invention can also  
CC be used for detecting a predisposition to, differentiation between  
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
CC haematopoietic cell proliferative disorders. The present method enables a  
CC highly specific classification of haematopoietic cell proliferative  
CC disorders allowing for improved and informed treatment of patients

Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 8; Length 2932;  
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CCAGCATCTCCAGAGCAGAGTT 25  
1594 CCAGCATCTCCAGAGCAGAGTT 1570

RESULT 4  
ADB53945/c  
ID ADB53945 standard; DNA; 2932 BP.  
AC ADB53945;  
XX 04-DEC-2003 (first entry)  
DT 04-DEC-2003 (first entry)  
XX MDR1 genomic DNA region.  
DE colon cell proliferative disorder; non methylated CpG dinucleotide;  
XX cytosine; cancer; adenoma; carcinoma; cytosine methylation state; da.  
KM Unidentified.  
XX WO2003072821-A2.  
FN 04-SEP-2003.  
XX 27-FEB-2003; 2003WO-EP002035.  
PF 27-FEB-2002; 2002EP-00004551.  
XX (EPIG-) EPIGENOMICS AG.  
PA Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Leesche R;  
XX Rujan T, Schmitt A;  
PI WPI; 2003-731620/69.  
XX  
XX Detecting and differentiating between colon cell proliferative disorders  
XX associated with a gene or its regulatory regions comprising contacting a  
XX target nucleic acid in a biological sample obtained from the subject with  
XX a reagent.  
XX Claim 46; SEQ ID NO 1; 74bp; English.  
XX The invention relates to a novel method for detecting and differentiating  
XX between colon cell proliferative disorders associated with at least one  
XX gene or its regulatory regions. The method comprises contacting a target  
XX nucleic acid in a biological sample obtained from the subject with at

least one reagent or a series of reagents, where the reagent or series of  
CC reagents, distinguishes between methylated and non methylated CpG  
CC dinucleotides within the target nucleic acid. The molecules of the  
CC invention demonstrate cytosine activity whilst the method may useful  
CC for detecting and differentiating between colon adenoma and colon carcinoma.  
CC disorders, including cancers such as colon adenoma and colon carcinoma.  
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for  
CC determining cytosine methylation state or single nucleotide  
CC polymorphisms. The current sequence is that of the genomic DNA region of  
CC the invention. This sequence is not shown within the specification but is  
CC taken from Wipoweb.

Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 10; Length 2932;  
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CCAGCATCTCCAGAGCAGAGTT 25  
1594 CCAGCATCTCCAGAGCAGAGTT 1570

RESULT 5  
ADEB84005/c  
ID ADEB84005 standard; DNA; 2932 BP.  
AC ADEB84005;  
XX 29-JAN-2004 (first entry)  
DT 5' regulatory region of human gene MDR1.  
XX

de; lymphoid cell proliferative disorder; methylation;  
XX methylated CpG dinucleotide; single nucleotide polymorphism; SNP;  
XX diffuse large B-cell lymphoma; mantle cell lymphoma;  
XX chronic lymphocytic leukemia; small lymphocytic lymphoma;  
XX follicular lymphoma; diagnosis; prognosis.

XX Homo sapiens.  
XX WO2003044226-A2.  
XX 30-MAY-2003.  
XX 25-NOV-2002; 2002WO-EP013265.  
XX 23-NOV-2001; 2001DE-01057491.  
XX 28-DEC-2001; 2001DE-01064501.  
XX (EPIG-) EPIGENOMICS AG.

Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimrich I;  
XX WPI; 2003-457621/43.  
XX  
XX Detecting and differentiating between lymphoid cell proliferative  
XX disorders comprising contacting a target nucleic acid with at least one  
XX reagent that distinguishes between methylated and non-methylated CpG  
XX dinucleotides.

Disclousure; SEQ ID NO 1; 448bp; English.  
XX The invention relates to a method of detecting and differentiating  
XX between lymphoid cell proliferative disorders associated with at least  
XX one gene and/or their regulatory regions in a subject by contacting a  
XX target nucleic acid in a biological sample obtained from the subject with  
XX at least one reagent or series of reagents that distinguish between  
XX methylated and non-methylated CpG dinucleotides within the target nucleic  
XX acid. The genes and/or their regulatory regions are preferably selected  
XX from MDR1, GSK2B, EGR4, AR, CDK4, RB2, CDC25A, Grib beta, MYO1, CDH3,  
XX MYC1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,  
XX GSP11, HIC-1, MGMT, MHL1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C,

CC GSK3beta, ESR1, APAF1, BAX, BAX or HOXA5. Oligomers, peptide nucleic  
 CC acid (PNA)-oligomers and/or isolated nucleic acid based on the sequences  
 CC of the genes are useful for detecting the methylation state of all the  
 CC CpG dinucleotides within one or more the sequences, or their complements,  
 CC for determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs), and for differentiating at least two of the medical  
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,  
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular  
 CC lymphoma. They are also useful for detecting of a predisposition to,  
 CC differentiation between subtypes, diagnosis, prognosis, treating and/or  
 CC monitoring of lymphoid cell proliferative disorder. This sequence  
 CC represents the 5' and/or regulatory region from one of the above  
 CC mentioned genes.

XX Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 2932;  
 Best Local Similarity 100.0%; Pred. No. 0.36;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGGAGCAGAGTT 25  
 |||||  
 Db 1594 CCAGCATCTCCAGGAGCAGAGTT 1570

RESULT 6  
 ADS88985/c  
 ID ADS88985 standard; DNA; 2932 BP.

XX ADS88985;  
 XX 18-NOV-2004 (first entry)  
 XX Human ABCB1 gene SEQ ID NO:1.

XX de; gene; human; cell proliferative disorder; breast; methylation;  
 KM cytosine; gene therapy; single nucleotide polymorphism; SNP.

XX Homo sapiens.

PN WO2004035803-A2.

XX 29-APR-2004.

PF 01-OCT-2003; 2003WO-EP010881.

PR 01-OCT-2002; 2002DE-01045779.

PR 07-JAN-2003; 2003DE-01000696.

PR 17-APR-2003; 2003DE-01017955.

PA (EPIG-) EPIGENOMICS AG.

PI Poekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F,

PI Mimmich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;

DR WPI; 2004-348468/32.

XX Predicting responsiveness of a subject with breast cell proliferative

XX disorder, useful for treating or differentiating breast cell

XX proliferative disorders comprises analyzing methylation pattern of a

XX genomic DNA from the subject.

XX Example 2; SEQ ID NO 1; 104pp; English.

XX The invention relates to a novel method for predicting the responsiveness  
 CC of a subject with a cell proliferative disorder of the breast tissues to  
 CC a therapy comprising analyzing the methylation pattern of a target  
 CC nucleic acid by contacting at least one of the target nucleic acids in a  
 CC biological sample obtained from the subject prior to or during treatment.  
 CC The method of the invention has cytosine activity, and may have a use  
 CC in gene therapy. The set of oligonucleotides comprising at least two of  
 CC the oligomers are useful for detecting the cytosine methylation state  
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The

CC methods, nucleic acid, oligonucleotide, and kit are useful for the  
 CC treatment, characterization, classification and/or differentiation, of  
 CC breast cell proliferative disorder. The method is also useful for  
 CC predicting the responsiveness of a subject with a cell proliferative  
 CC disorder of the breast tissues to a therapy. The present sequence is used  
 CC in the exemplification of the invention.

XX Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 2932;  
 Best Local Similarity 100.0%; Pred. No. 0.36;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGGAGCAGAGTT 25  
 |||||  
 Db 1594 CCAGCATCTCCAGGAGCAGAGTT 1570

RESULT 7  
 ABS98184/c  
 ID ABS98184 standard; DNA; 8573 BP.

XX ABS98184;

XX 23-DEC-2002 (first entry)

XX Human multidrug resistance gene promoter B and exons 1-3 sequence.

XX Human; de; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR12;

XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

XX HMGR; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

XX NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase thermolabile;

XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; UPA;

XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

XX multidrug resistance associated protein 3; cancer; prostate;

XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR5;

XX altered drug metabolism; cardiovascular function; colorectal tumour;

XX central nervous system; pulmonary; immunological; SNP;

XX single nucleotide polymorphism.

XX Homo sapiens.

PN WO200257410-A2.

XX 25-JUL-2002.

PF 28-NOV-2001; 2001WO-US044838.

PR 28-NOV-2000; 2000US-00724389.

PA (DNAS-) DNA SCI LAB INC.

PI Guida M, Hall J;

DR WPI; 2002-698522/75.

XX Isolated nucleic acid molecules having polymorphisms in known human genes  
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
 PT for locating, identifying and characterizing the genes responsible for  
 PT disorder-related traits.

XX Example 22; Page 432-437; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),

CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), dizepam binding  
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
 CC transferase (HNMT), [kallikrein 2] KLK2, nicotinamide-N-methyl  
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
 CC sulfolipase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (uPAR), multidrug resistance 1  
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterizing the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorder. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1,  
 CC ANMT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB3 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HNMT for altered pulmonary,  
 CC immunological or haematological function, in KLK2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC polymorphic DNA sequence of the invention

SO Sequence 8573 BP; 2739 A; 1422 C; 1705 G; 2707 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 8573;  
 Best Local Similarity 100.0%; Pred. No. 0.41;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25  
 Db 2539 CCAGCATCTCCAGCAGGACAGATT 2515

# RESULT 8

ADD41243/C  
 ID ADD41243 standard; DNA; 10200 BP.

XX ADD41243;

DT 30-OCT-2002 (first entry)

XX Human MDR1 gene 5' flanking region.

XX Human, transgenic; reporter construct; CYP3A4; cytochrome P450;  
 KW transcriptional regulatory element; xenobiotic; steroid; MDR1;  
 KW p-glycoprotein; gene; de.

OS Homo sapiens.

XX WO200236784-A1.

XX 10-MAY-2002.

XX 01-NOV-2001; 2001WO-AU001407.

XX 01-NOV-2000; 2000AU-00001161.

XX 10-MAY-2001; 2001AU-00004901.

XX (UNSY ) UNIV SYDNEY.  
 XX Liddle C, Goodwin BJ, Robertson G,  
 PI

XX MPI; 2002-537301/57.

DR Non-human mammal for determining the effect of a compound on regulation  
 PT of CYP3A4 gene expression, comprises a reporter construct for producing a  
 PT reporter linked to a transcriptional regulatory nucleic acid from a human  
 PT CYP3A4 gene.

PS Claim 11; Page 83-92; 95pp; English.

XX The invention relates to generation of non-human transgenic animals  
 CC comprising a reporter construct for producing a detectable amount of a  
 CC reporter molecule operably linked to a transcriptional regulatory nucleic  
 CC acid molecule from the human CYP3A4 gene. The invention also relates to  
 CC transgenic animal for analysing CYP3A4 cytochrome P450 gene regulation.  
 CC The non-human mammal of the invention is useful for determining whether a  
 CC compound is capable of effecting the transcription of a human CYP3A4  
 CC gene. It is also useful for determining the effect of a compound such as  
 CC a xenobiotic or steroid on the regulation of expression of the CYP3A4  
 CC gene in a human. The present sequence is 5' flanking region of human (p-  
 CC glycoprotein) MDR1 gene. This sequence is used as a regulatory element in  
 CC the invention

SO Sequence 10200 BP; 3296 A; 1785 C; 1985 G; 3134 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 10200;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25  
 Db 9817 CCAGCATCTCCAGCAGGACAGATT 9793

# RESULT 9

ACF62751/C  
 ID ACF62751 standard; DNA; 177380 BP.

XX ACF62751;

DT 08-OCT-2003 (first entry)

XX Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.

XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;  
 KW cytochrome P450; subfamily IIA; nifedipine oxidase; polypeptide 5;  
 KW cytosolic; gene; de.

XX Unidentified.

XX WO2003013534-A2.

XX 20-FEB-2003.

XX 23-JUL-2002; 2002WO-EP008219.

XX 23-JUL-2001; 2001EP-00117608.

XX 24-MAY-2002; 2002EP-00011710.

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX Heinrich G, Korb R,

XX MPI; 2003-268144/26.

XX New use of irinotecan for preparation of compositions for treating cancer  
 PT in subject having genome with variant allele comprising cytochrome P450,  
 PT subfamily IIA, polypeptide 5 polynucleotide, termed CYP3A5.

XX Disclosure; SEQ ID NO 683; 86pp; English.

XX The present invention describes the use of irinotecan (I) or its  
 CC derivative for the preparation of a pharmaceutical composition for

CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject having a genome with a variant  
 CC allele which comprises a cytochrome p450, subfamily I11A (rifedione  
 CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have  
 CC cytostatic activity. The therapeutic applications of (I) is improved,  
 CC since it is possible to individually treat a subject with an appropriate  
 CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,  
 CC harmful or toxic effects are efficiently avoided. Unnecessary and  
 CC potentially harmful treatment of those subjects who do not respond to the  
 CC treatment with substances (nonresponders), as well as the development of  
 CC drug resistances due to suboptimal drug dosing can be avoided. ACP62200  
 CC to ACP62751 and ABM34912 to ABM35013 represent sequences used in the  
 CC exemplification of the present invention

XX  
 SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 177380;  
 Best Local Similarity 100.0%; Pred. No. 0.61;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCAGCATCTCCAGGAGGAGGAGTT 25  
 DB 141346 CCAGCATCTCCAGGAGGAGGAGTT 141322

RESULT 10  
 ADB20870/c  
 ID ADB20870 standard; DNA; 177380 BP.

XX  
 AC ADB20870;

XX  
 DT 20-NOV-2003 (first entry)

XX  
 DE MRP1 based cancer related nucleic acid SEQ ID NO:683.

XX  
 KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
 KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
 KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;  
 KW ds.

XX  
 OS Unidentified.

XX  
 PN WO2003013533-A2.

XX  
 PD 20-FEB-2003.

XX  
 PF 23-JUL-2002; 2002MO-EP008200.

XX  
 PR 23-JUL-2001; 2001EP-00117608.

XX  
 PR 24-MAY-2002; 2002EP-00011710.

XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX  
 PI Heinrich G, Kerb R;

XX  
 DR WPI; 2003-354397/33.

XX  
 PT Use of irinotecan or its derivative for preparation of a pharmaceutical  
 PT composition for treating cancer in a subject having a genome with a  
 PT variant allele comprising a multidrug resistance protein 1  
 PT polynucleotide.

XX  
 PS Disclosure; SEQ ID NO 683; 100bp; English.

XX  
 CC The present invention describes a method for the use of irinotecan (I) or  
 CC its derivative for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject having a genome with a variant  
 CC allele which comprises a multidrug resistance protein 1 (MRP1)  
 CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative  
 CC can be used for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject, where the subject is a human

CC (preferably African or Asian) or a mouse. The present sequence represents  
 CC a sequence which is used in the exemplification of the present invention.

XX  
 SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 177380;  
 Best Local Similarity 100.0%; Pred. No. 0.61;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCAGCATCTCCAGGAGGAGGAGTT 25  
 DB 141346 CCAGCATCTCCAGGAGGAGGAGTT 141322

RESULT 11  
 ADB87959/c  
 ID ADB87959 standard; DNA; 177380 BP.

XX  
 AC ADB87959;

XX  
 DT 04-DEC-2003 (first entry)

XX  
 DE Human UGT1A1 gene sequence SEQ ID NO:683.

XX  
 KW irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;  
 KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;  
 KW ovarian cancer; pancreatic cancer; malignant glioma;  
 KW uridine diphosphate glycosyltransferase member A1; gene; ds.

XX  
 OS Homo sapiens.

XX  
 PN WO2003013536-A2.

XX  
 PD 20-FEB-2003.

XX  
 PF 23-JUL-2002; 2002MO-EP008217.

XX  
 PR 23-JUL-2001; 2001EP-00117608.

XX  
 PR 24-MAY-2002; 2002EP-00011710.

XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX  
 PI Heinrich G, Kerb R;

XX  
 DR WPI; 2003-289896/28.

XX  
 PT Use of irinotecan to treat cancer patient by determining if patient has  
 PT variant alleles of UGT1A1 gene, administering increased/decreased amounts  
 PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.

XX  
 PS Disclosure; SEQ ID NO 683; 107bp; English.

XX  
 CC The invention relates to the novel use of irinotecan to treat a patient  
 CC suffering from cancer. This involves determining if the patient has one  
 CC or more variant alleles of the UGT1A1 gene, and if the patient has one  
 CC or more of such variant alleles, irinotecan is administered in an increased  
 CC or decreased amount in comparison to the amount that is administered  
 CC without regard to the patient's alleles in the UGT1A1 gene. The invention  
 CC has cytostatic activity. A composition of the invention acts as a  
 CC topoisomerase I inhibitor. The method is useful for treating a patient,  
 CC an animal e.g. mouse or a human, preferably African or Asian, suffering  
 CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,  
 CC pancreatic cancer or malignant glioma. The present sequence is used in  
 CC the exemplification of the invention.

XX  
 SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 177380;  
 Best Local Similarity 100.0%; Pred. No. 0.61;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCAGCATCTCCAGGAGGAGGAGTT 25  
 DB 141346 CCAGCATCTCCAGGAGGAGGAGTT 141322

DB 141346 CCAGCATCTCCAGCAGGAGGATT 141322

RESULT 12

ADB96942/c

ID ADB96942 standard; DNA; 177380 BP.

XX ADB96942;

AC

XX 04-DEC-2003 (first entry)

DT

XX Human MDR1 related DNA sequence SEQ ID NO:683.

DE

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

KM multidrug resistance 1; MDR1; cytosolic; human; CYP3A5; MRP1; MDR1;

KM TOP1; ds.

XX Homo sapiens.

OS

XX WO2003013537-A2.

PN

XX 20-FEB-2003.

PD

XX 23-JUL-2002; 2002WO-EP008218.

PE

XX 23-JUL-2001; 2001EP-00117608.

PR

XX 24-MAY-2002; 2002EP-00011710.

PA

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PI

XX Heinrich G, Kerb R;

XX WPI; 2003-268145/26.

DR

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; SEQ ID NO 683; 130pp; English.

XX

XX The invention relates to the novel use of irinotecan or its derivative

CC for the preparation of pharmaceutical compositions for treating

CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or

CC malignant glioma in a subject having a genome with a variant allele which

CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition

CC of the invention has cytostatic activity. The invention is useful for the

CC preparation of pharmaceutical compositions for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject (preferably human, more preferably African or Asian)

CC or a mouse. The present sequence is used in the exemplification of the

CC invention.

XX

XX Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

XX

XX

XX Query Match 100.0%; Score 25; DB 10; Length 177380;

XX Best Local Similarity 100.0%; Pred. NO. 0.61;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 CCAGCATCTCCAGCAGGAGGATT 25

DB 141346 CCAGCATCTCCAGCAGGAGGATT 141322

RESULT 13

ADB92133/c

ID ADB92133 standard; DNA; 177380 BP.

XX

XX ADB92133;

AC

XX 04-DEC-2003 (first entry)

DT

XX Human MDR1 related DNA sequence SEQ ID NO:683.

DE

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

KM multidrug resistance 1; MDR1; cytosolic; human; UGT1A1; MRP1; TOP1; ds.

XX Homo sapiens.

OS

XX WO2003013535-A2.

PN

XX 20-FEB-2003.

PD

XX 23-JUL-2002; 2002WO-EP008220.

PE

XX 23-JUL-2001; 2001EP-00117608.

PR

XX 24-MAY-2002; 2002EP-00011710.

PA

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PI

XX Heinrich G, Kerb R;

XX WPI; 2003-342400/32.

DR

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; SEQ ID NO 683; 104pp; English.

XX

XX The invention relates to a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the

CC invention has cytostatic activity. The present sequence is used in the

CC exemplification of the invention.

XX

XX Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

XX

XX

XX Query Match 100.0%; Score 25; DB 10; Length 177380;

XX Best Local Similarity 100.0%; Pred. NO. 0.61;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 CCAGCATCTCCAGCAGGAGGATT 25

DB 141346 CCAGCATCTCCAGCAGGAGGATT 141322

RESULT 14

ABN37191/c

ID ABN37191 standard; DNA; 60 BP.

XX

XX ABN37191;

AC

XX 15-JUL-2002 (first entry)

DT

XX Human spliced transcript detection oligonucleotide SEQ ID NO:9939.

DE

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KM Human variant; transcriptome; oligonucleotide library; ss.

KM

XX Homo sapiens.

OS

XX WO200210449-A2.

PN

XX 07-FEB-2002.

PD

XX 20-JUL-2001; 2001WO-1B001903.

PE

XX 28-JUL-2000; 2000US-0221607P.

PR

XX 02-MAY-2001; 2001US-0287724P.

PA

XX (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 9939; 47bp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini-  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 60 BP; 16 A; 15 C; 16 G; 13 T; 0 U; 0 Other;  
 Query Match 74.4%; Score 18.6; DB 6; Length 60;  
 Best Local Similarity 84.0%; Pred. No. 1.6e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CCAGCATCTCCAGCAGGCGAGCTT 25  
 Db 36 CCAGCAGCTCCAGCAGGCGTCACTT 12  
 RESULT 15  
 ID ADO44565 standard; DNA; 354 BP.  
 XX  
 AC ADO44565;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AI480570expressed sequence tag (EST) fragment.  
 XX  
 KM CRH; corticotropin-releasing hormone; antidepressant; tranquillizer;  
 KM gene therapy; CNS; expressed sequence tag; EST; ds.  
 XX  
 OS Mus sp.  
 XX  
 PN WO2004039837-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 23-OCT-2003; 2003WO-EP011792.  
 XX  
 PR 31-OCT-2002; 2002WO-EP012274.  
 XX  
 PA (JANC ) JANSSEN PHARM NV.  
 XX  
 PI Peeters PJ, Goehlmann HH, Swagemakers SMA, Kass SU, Steckler THW,  
 PI Fierens FLP;

XX  
 DR WPI; 2004-376160/35.  
 DR GENBANK; AI848545.  
 XX  
 PT Diagnosing a corticotropin-releasing hormone (CRH)-induced gene  
 PT expression profile in an individual comprises determining polypeptides  
 PT and polynucleotides that mediate the endocrine response to CRH in the  
 PT sample.  
 XX  
 PS Claim 1; SEQ ID NO 31; 84bp; English.  
 XX  
 CC The invention relates to diagnosing a corticotropin-releasing hormone  
 CC (CRH)-induced gene expression profile in an individual. The method  
 CC involves determining the level of gene transcription of a gene comprising  
 CC a nucleic acid sequence selected from 28 nucleotide sequences fully  
 CC defined in the specification or determining the amount of at least one  
 CC protein that modulates CRH signaling in the sample, where the protein  
 CC comprises 13 amino acid sequences given in the specification. The methods  
 CC and composition are useful for diagnosing, treating and/or preventing CRH  
 CC metabolism-related disorders, such as CRH-induced depression or stress.  
 CC The polynucleotide is used as a marker of CRH signaling in a cell. These  
 CC composition and methods may also be used in identifying compounds that  
 CC modulate CRH-induced depression and stress. The present sequence  
 CC represents a specific example of a gene fragment that is an important  
 CC mediator of CRH-induced changes in the CNS.  
 XX  
 SQ Sequence 354 BP; 107 A; 71 C; 68 G; 108 T; 0 U; 0 Other;  
 Query Match 74.4%; Score 18.6; DB 12; Length 354;  
 Best Local Similarity 84.0%; Pred. No. 2e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CCAGCATCTCCAGCAGGCGAGCTT 25  
 Db 262 CCAGCAGCTCCAGCAGGCGTCACTT 286

Search completed: February 9, 2005, 16:05:56  
 Job time : 247.69 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds  
(without alignments)  
388.593 Million cell updates/sec

Title: US-10-007-255-11

Perfect score: 1 cccagcatctccacgaagcagcagct 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_scc1.\*  
2: gb\_scc2.\*  
3: gb\_hlc.\*  
4: gb\_scc3.\*  
5: gb\_scc4.\*  
6: gb\_scc5.\*  
7: gb\_scc6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20.2	80.8	505	1	AV631826
2	20.2	80.8	514	1	AV626483
3	20.2	80.8	702	8	BZ536972
4	20.2	80.8	724	9	CG206154
5	20.2	80.8	852	9	CG436506
6	20.2	80.8	893	8	BZ785280
7	20.2	80.8	955	9	CG436517
8	19.8	79.2	550	4	BM257699
9	19.8	79.2	584	1	AL726135
10	19.8	79.2	585	5	BX307891
11	19.8	79.2	597	1	AL726201
12	19.8	79.2	598	1	AV594929
13	19.8	79.2	680	5	BX299583
14	19.8	79.2	687	7	CR364140
15	19.8	79.2	778	7	CN069432
16	19.2	76.8	390	6	C82708
17	19.2	76.8	390	6	C83564
18	19.2	76.8	451	8	B83634
19	19.2	76.8	481	8	AZ840094
20	19.2	76.8	561	6	CD211773
21	19.2	76.8	573	7	CK755307
22	19.2	76.8	575	7	CO997477
23	19.2	76.8	619	9	FR000396
24	19.2	76.8	627	6	BY722128

25	19.2	76.8	652	8	AZ429284
26	19.2	76.8	655	8	AZ362097
27	19.2	76.8	677	6	CD916489
28	19.2	76.8	748	9	CC576251
29	19.2	76.8	1202	3	AK020597
30	19.2	76.8	244	4	BI403715
31	18.8	75.2	459	2	BF740661
32	18.8	75.2	580	6	CA501097
33	18.8	75.2	591	7	AZ717777
34	18.8	75.2	595	7	CF180183
35	18.8	75.2	851	8	BH516844
36	18.8	75.2	909	4	BI772691
37	18.6	74.4	171	8	AQ012740
38	18.6	74.4	226	2	BE717844
39	18.6	74.4	232	2	BF932509
40	18.6	74.4	245	2	BE827704
41	18.6	74.4	281	1	AV102388
42	18.6	74.4	289	1	AA990519
43	18.6	74.4	313	2	BE837783
44	18.6	74.4	320	2	BE717759
45	18.6	74.4	321	4	BG074771

## ALIGNMENTS

RESULT 1  
AV631826 505 bp mRNA linear EST 15-DEC-2000  
DEFINITION AV631826 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LC100d12\_r 5', mRNA sequence.

AV631826 GI:10794460  
EST.  
Chlamydomonas reinhardtii  
Chlamydomonas reinhardtii  
Bukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 505)  
Asamizu,E., Mura,K., Kuchio,K., Inoue,Y., Fukuzawa,H., Ohnaka,K., Nakamura,Y. and Tabata,S.

Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii  
DNA Res. 7 (5), 305-307 (2000)

JOURNAL MEDLINE PUBMED  
11089912  
Contact: Erika Asamizu

The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

## FEATURES

source  
1..505  
/organism="Chlamydomonas reinhardtii"  
/mol\_type="mRNA"  
/strain="C9"  
/db\_xref="taxon:3055"  
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/note="Vector: plasmid pUC19 SK-; Site 1: EcoRI; Site 2: XhoI. The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"

## ORIGIN

Query Match 80.8% Score 20.2; DB 1; Length 505;  
Best local similarity 88.0%; Pred. No. 4.1e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCAGCATCTCCACGAAGCAGAGTT 25  
474 CCAGCATCTTCACAAATGCAGATT 498



RESULT 2  
AV626483  
LOCUS  
DEFINITION  
AV626483 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LCL009h12\_r 5', mRNA sequence.  
ACCESSION  
AV626483  
VERSION  
AV626483.1 GI:10780763  
KEYWORDS  
EST.  
SOURCE  
Chlamydomonas reinhardtii  
Chlamydomonas reinhardtii  
Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas.  
REFERENCE  
1 (bases 1 to 514)  
Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohya, K., Nakamura, Y., and Tabata, S.  
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii  
DNA Res. 7 (5), 305-307 (2000)  
COMMENT  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
FEATURES  
source  
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/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"  
ORIGIN  
Query Match 80.8%; Score 20.2; DB 1; Length 514;  
Best Local Similarity 88.0%; Pred. No. 4.1e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCACGAGGCGAGATT 25  
Db 463 CCAGCATCTTCACAAATGCAGAGTT 487  
RESULT 3  
BZ536972  
LOCUS  
DEFINITION  
BZ536972 702 bp DNA linear GSS 16-DEC-2002  
OGAH187C ZM2.0.7.1.5 KB Zea mays genomic clone ZMMEM061C12, genomic survey sequence.  
ACCESSION  
BZ536972  
VERSION  
BZ536972.1 GI:27085170  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 702)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Buddiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@cigr.org  
Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers  
1..702  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
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/clone\_1lb="ZM2.0.7.1.5 KB"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"  
ORIGIN  
Query Match 80.8%; Score 20.2; DB 8; Length 702;  
Best Local Similarity 88.0%; Pred. No. 4.3e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCACGAGGCGAGATT 25  
Db 238 CCAGCATCTGCACGAGCGCAAGTT 262  
RESULT 4  
CG206154  
LOCUS  
DEFINITION  
CG206154 724 bp DNA linear GSS 21-AUG-2003  
PUDB60TD ZM.0.6.1.0 KB Zea mays genomic clone ZMMBT0640J24, genomic survey sequence.  
ACCESSION  
CG206154  
VERSION  
CG206154.1 GI:34097215  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 724)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.  
Maize Genomics Consortium  
Unpublished (2003)  
Other GSSes: PUDB60TB  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@cigr.org  
Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high COT selected genomic DNA library"  
ORIGIN  
Query Match 80.8%; Score 20.2; DB 9; Length 724;  
Best Local Similarity 88.0%; Pred. No. 4.3e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCAGCATCTCCACGAGGCGAGATT 25  
Db 367 CCAGCATCTGCACGAGCGCAAGTT 343



RESULT 5  
CG436506  
LOCUS  
DEFINITION OGVGE10TH ZM 0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0475A19,  
genomic survey sequence.  
ACCESSION CG436506  
VERSION CG436506.1 GI:34813045  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 852)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGVGE10TV  
Contact: Cathy Whitelaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 80.8%; Score 20.2; DB 9; Length 852;  
Best Local Similarity 88.0%; Pred. No. 4.4e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCAAGATT 25  
|||  
Db 818 CCAGCATCTGCACGAGGCAAGATT 842

RESULT 6  
B2785280/c  
LOCUS B2785280 893 bp DNA linear GSS 17-MAR-2003  
DEFINITION PUPAX84TB ZM 0.6\_1.0\_KB Zea mays genomic clone ZMMBTa277N24,  
genomic survey sequence.  
ACCESSION B2785280  
VERSION B2785280.1 GI:28978877  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 893)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,F., Ma,J. and  
Bennetzen,J.  
Maize Genomics Consortium  
Unpublished (2003)  
Contact: Cathy Whitelaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..893  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1lb="ZM 0.6\_1.0\_KB"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

ORIGIN  
Query Match 80.8%; Score 20.2; DB 8; Length 893;  
Best Local Similarity 88.0%; Pred. No. 4.5e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCAAGATT 25  
|||  
Db 415 CCAGCATCTGCACGAGGCAAGATT 391

RESULT 7  
CG436517/c  
LOCUS CG436517 955 bp DNA linear GSS 17-SEP-2003  
DEFINITION OGVGE10TV ZM 0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0475A19,  
genomic survey sequence.  
ACCESSION CG436517  
VERSION CG436517.1 GI:34813056  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 955)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGVGE10TH  
Contact: Cathy Whitelaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers  
1..955  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1lb="ZM 0.7\_1.5\_KB"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 80.8%; Score 20.2; DB 9; Length 955;  
Best Local Similarity 88.0%; Pred. No. 4.5e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCAAGATT 25  
|||  
Db 310 CCAGCATCTGCACGAGGCAAGATT 286

RESULT 8  
BM257699/c 550 bp mRNA linear EST 17-DEC-2001

LOCUS BM257699  
DEFINITION 521522 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.  
ACCESSION BM257699  
VERSION BM257699.1 GI:17893298  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 550)  
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cabaas, E., Wray, J.E., White, J., Cho, J.W., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Perera, G., Holt, I., Karamycheva, S., Llang, F., Quackenbush, J., and Keefe, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smtlth@mail.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -mnscore 18 and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAAACGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGAG  
Plate: 125 row: D column: 5  
Seq. primer: ATTAGCTGACACTATG.  
Location/Qualifiers  
1..550  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3BOV"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

ORIGIN

Query Match 79.2%; Score 19.8; DB 4; Length 550;  
Best Local Similarity 91.3%; Pred. No. 6.2e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGCAGGACGAG 23  
122 CCAGCAGCTCCAGCAGGCTGAG 100

Db 122 CCAGCAGCTCCAGCAGGCTGAG 100

RESULT 9  
AL726135 584 bp mRNA linear EST 18-APR-2002

LOCUS AL726135  
DEFINITION AL726135 Danio rerio embryonic inner ear substracted CDNA Danio  
terio cDNA clone BN0A083ZH02 5', mRNA sequence.  
ACCESSION AL726135  
VERSION AL726135.1 GI:20190739  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 584)  
Coimbra, R., Weil, D., Brothier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J., and Petit, C.  
A substracted CDNA library from the zebrafish (Danio rerio) embryonic inner ear  
Unpublished (2002)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1..584  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="BN0A083ZH02"  
/tissue\_type="inner ear"  
/dev\_stage="embryonic"  
/clone\_lib="Danio rerio embryonic inner ear substracted CDNA"  
/note="substracted CDNA library"

ORIGIN

Query Match 79.2%; Score 19.8; DB 1; Length 584;  
Best Local Similarity 91.3%; Pred. No. 6.3e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCATCTCCAGCAGGACGAGTT 25  
299 AGCATCTCCAGCAGGACGAGTT 321

Db 299 AGCATCTCCAGCAGGACGAGTT 321

RESULT 10  
BX307891 585 bp mRNA linear EST 11-MAY-2004

LOCUS BX307891 tcaay Oncorhynchus mykiss CDNA clone tcaay0016b.m.17 5prim,  
DEFINITION mRNA sequence.  
ACCESSION BX307891  
VERSION BX307891.2 GI:42616971  
KEYWORDS EST.  
SOURCE Oncorhynchus mykiss (rainbow trout)  
ORGANISM Oncorhynchus mykiss

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 585)  
Govoroun, M., Guiguen, Y., and Le Gac, F.  
Construction and primary characterization of normalized CDNA libraries in rainbow trout, Oncorhynchus mykiss  
Unpublished (2003)  
On Apr 7, 2003 this sequence version replaced gi:29588536.  
Contact: Guiguen Y  
INRA - SCRIBE  
Campus de beaulieu, RENNES cedex, 35042, France  
Tel: 02.23.48.50.09  
Fax: 02.23.48.50.20  
Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenauporte@jouy.inra.fr to obtain the chromatogram of this sequence.  
Plate: 0016 row: m column: 17  
Seq primer: M13r.  
Location/Qualifiers  
1..585  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/db\_xref="taxon:8022"  
/clone="tcaay0016b.m.17"  
/tissue\_type="adipose tissue, blood, brain, differentiating gonads, gills, interrenal, intestine, kidney, liver, muscle, ovary, pituitary, testis"

FEATURES  
Source

/dev\_stage="from embryos to adults"  
 /lab\_host="DH10B"  
 /clone\_lib="lccay"  
 /note="Vector: pT7T3D-Pac; Rainbow trout multi-tissues -  
 normalized + 1 subtraction (lccay) ; Clone distribution :  
 AGNNAE Resource centre, Francois PIMM,  
 Francois.Pimmi@jouy.inra.fr, INRA, CEA Radiobiologie et  
 Etude du genome (LREG), Domaine de Vilvert, 78352,  
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33  
 (0) 1.34.65.22.73"

## ORIGIN

Query Match 79.2%; Score 19.8; DB 5; Length 585;  
 Best Local Similarity 91.3%; Pred. No. 6.3e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAGCATCTCCAGAGGACAGGT 24  
 |||||  
 Db 82 CACCATCTCCAGAGGACAGGT 60

RESULT 11  
 AL726201/c 587 bp mRNA linear EST 18-APR-2002

LOCUS AL726201 Danio rerio embryonic inner ear subtracted cDNA Danio  
 DEFINITION rerio cDNA clone BNOA0832H02.3, mRNA sequence.

ACCESSION AL726201 GI:20190805

VERSION EST

KEYWORDS Danio rerio (zebrafish)

ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

## REFERENCE

## AUTHORS

Colimba, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,  
 Hardekin, J.P., Weissenbach, J. and Petit, C.  
 A subtracted cDNA library from the zebrafish (Danio rerio)

## JOURNAL

embryonic inner ear  
 Unpublished (2002)  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE.  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

## FEATURES

## SOURCE

1..587  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="BNOA0832H02"  
 /tissue\_type="inner ear"  
 /dev\_stage="embryonic"  
 /clone\_lib="Danio rerio embryonic inner ear subtracted  
 cDNA"  
 /note="subtracted cDNA library"

## ORIGIN

Query Match 79.2%; Score 19.8; DB 1; Length 587;  
 Best Local Similarity 91.3%; Pred. No. 6.3e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCATCTCCAGAGGACAGATT 25  
 |||||  
 Db 289 AGCATCTCCAGAGGACAGATT 267

## RESULT 12

## LOCUS

AVS94929 595 bp mRNA linear EST 27-NOV-2001  
 AVS94929 Bos taurus cartilage fetus Bos taurus cDNA clone

## DEFINITION

## ACCESSION

AVS94929  
 AVS94929.1 GI:9711387

KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.

## REFERENCE

1 (bases 1 to 595)  
 Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.  
 and Sugimoto, Y.  
 Establishment of a high throughput EST sequencing system using  
 poly(A) tail-removed cDNA libraries and determination of 36,000  
 bovine ESTs

## TITLE

Nucleic Acids Res. 29 (22), E108 (2001)

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

11713328  
 Contact: Yoshikazu Sugimoto  
 Animal Genetics Division  
 Shikawa Institute of Animal Genetics  
 Oakura, Nishigo, Nishi-shikawa, Fukushima 961-8061, Japan  
 Tel: 81-248-25-5641  
 Fax: 81-248-25-5725  
 Email: kazusugi@cocoa.ocn.ne.jp  
 Single pass sequencing.  
 This clone was obtained from a polyA-deleted cDNA library.  
 Location/Qualifiers

## FEATURES

## SOURCE

1..595  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="EICA016F04"  
 /tissue\_type="cartilage"  
 /dev\_stage="fetus"  
 /lab\_host="DH10B"  
 /clone\_lib="Bos taurus cartilage fetus"  
 /note="Vector: pZLI; Site\_1: SalI; Site\_2: NotI; Poly A  
 was deleted from a NotI site"

## ORIGIN

Query Match 79.2%; Score 19.8; DB 1; Length 595;  
 Best Local Similarity 91.3%; Pred. No. 6.3e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGACAG 23  
 |||||  
 Db 223 CCAGCATCTCCAGAGGACAG 201

## RESULT 13

## LOCUS

BX299583 680 bp mRNA linear EST 10-MAY-2004  
 BX299583 tccay Oncorhynchus mykiss cDNA clone tccay0004b.1.10 5prim,  
 mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## ORGANISM

Oncorhynchus mykiss (rainbow trout)  
 Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

## REFERENCE

1 (bases 1 to 680)  
 Goyoroun, M., Guiguen, Y. and Le Gac, F.  
 Construction and primary characterization of normalized cDNA  
 libraries in rainbow trout, Oncorhynchus mykiss  
 Unpublished (2003)

## JOURNAL

## COMMENT

## CONTACT

On Apr 7, 2003 this sequence version replaced gi:29580228.  
 Contact: Guiguen Y  
 INRA - SCRIBR  
 Campus de Beaulieu, RENNES cedex, 35042, France  
 Tel: 02.23.48.50.09  
 Fax: 02.23.48.50.20  
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us

at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

Plate: 0004 row: 1 column: 10  
Seq primer: M13R.

# FEATURES

location/Qualifiers

1..680

/organism="Oncorhynchus mykiss"

/mol\_type="mRNA"

/db\_xref="taxon:8022"

/clone="tcab0004b.1.10"

/tissue\_type="adipose tissue, blood, brain,

differentiating gonads, gills, interrenal, intestine,

kidney, liver, muscle, ovary, pituitary, testis"

/dev\_stage="from embryos to adults"

/lab\_host="DH10B"

/clone\_lib="tcay"

/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues -

normalized + 1 subtraction (tcay) ; Clone distribution :

AGENAE Resource centre. Francois PIMET,

Francois Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et

Etude du genome (LREB), Domaine de Vilvert, 78352,

Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33

(0) 1.34.65.22.73"

## ORIGIN

Query Match 79.2%; Score 19.8; DB 5; Length 680;  
Best Local Similarity 91.3%; Pred. No. 6.4e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGAGGACAGT 24

Db 293 CACCATCTCCAGAGGACAGT 271

RESULT 14 CR364140 687 bp mRNA linear EST 21-APR-2004  
LOCUS CR364140 AGENAE Rainbow trout normalized testis library (tcbl)

DEFINITION Oncorhynchus mykiss cDNA clone tcbl0038c.j.24 5prim, mRNA sequence.

VERSION CR364140

KEYWORDS CR364140.1 GI:46475452

ORGANISM EST.

Oncorhynchus mykiss (rainbow trout)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 687)

Govoroun, M., Guiguen, Y. and Le Gac, F.

Construction and primary characterization of normalized cDNA

libraries in rainbow trout, Oncorhynchus mykiss

Unpublished (2003)

Contact: Guiguen Y

INRA - SCRIBE

Campus de Beaulieu, RENNES cedex, 35042, France

Tel: 02.23.48.50.09

Fax: 02.23.48.50.20

Email: Yann.Guiguen@beaulieu.rennes.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us

at sigenasupport@jouy.inra.fr to obtain the chromatogram of this

sequence.

Plate: 0038, row: 5 column: 24.

Seq primer: M13R.

location/Qualifiers

1..687

/organism="Oncorhynchus mykiss"

/mol\_type="mRNA"

/db\_xref="taxon:8022"

/clone="tcbl0038c.j.24"

/tissue\_type="testis"

/lab\_host="DH10B"

/clone\_lib="AGENAE Rainbow trout normalized testis library

(tcbl)"

## ORIGIN

Query Match 79.2%; Score 19.8; DB 7; Length 687;  
Best Local Similarity 91.3%; Pred. No. 6.5e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGAGGACAGT 24

Db 153 CACCATCTCCAGAGGACAGT 131

RESULT 15 CN069432 778 bp mRNA linear EST 30-MAR-2004  
LOCUS CN069432/c Salamander\_28\_M15.ab1 AG Ambystoma tigrinum tigrinum cDNA, mRNA

DEFINITION Salamander\_28\_M15.ab1 AG Ambystoma tigrinum tigrinum cDNA, mRNA

sequence.

ACCESSION CN069432

VERSION CN069432.1 GI:45833842

KEYWORDS EST.

ORGANISM Ambystoma tigrinum tigrinum (Eastern tiger salamander)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Ambipibia; Batrachia; Caudata; Salamandridae; Ambystomatidae;

Ambystoma.

1 (bases 1 to 778)

Putra, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D.,

Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Maness, N.J.,

Habermann, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Patchy, D.M.

and Voss, S.R.

From biomedicine to natural history research: EST resources for

ambystomatid salamanders

BMC Genomics 5 (1), 54 (2004)

Contact: SR Voss

Department of Biology

University of Kentucky

TH Morgan Building, Lexington, KY 40506, USA

Tel: 859 257 9888

Fax: 859 257 1717

Email: svoss@uky.edu

The EST is quality trimmed at the ends with a 20 base window and

quality threshold of 15 (phred quality score). Please visit

http://salamander.uky.edu for any information (trace, quality files

etc) regarding this EST.

location/Qualifiers

1..778

/organism="Ambystoma tigrinum tigrinum"

/mol\_type="mRNA"

/sub\_species="tigrinum"

/db\_xref="taxon:43116"

/tissue\_type="liver, lung, kidney, heart, gonad, brain and

gill tissues collected from metamorphosing larvae"

/clone\_lib="AG"

## ORIGIN

Query Match 79.2%; Score 19.8; DB 7; Length 778;  
Best Local Similarity 91.3%; Pred. No. 6.6e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAGCATCTCCAGAGGACAG 23

Db 646 CAGCATCTCCAGAGGACAG 624

Search completed: February 9, 2005, 21:55:37  
Job time : 2451.85 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-12

Perfect score: 1 agcttccaacacgctgaattccta 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_pl:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504309 Sequence
2	25	100.0	25	6	AX504326 Sequence
3	25	100.0	120	6	BD160755 Kit for a
4	25	100.0	120	6	BD160756 Kit for a
5	25	100.0	172	6	CQ110210 Sequence
6	25	100.0	172	6	CQ148922 Sequence
7	25	100.0	172	6	CQ232195 Sequence
8	25	100.0	172	6	CQ307508 Sequence
9	25	100.0	172	6	CQ344374 Sequence
10	25	100.0	201	11	BV202141
11	25	100.0	201	11	BV202142
12	25	100.0	209	9	HUMGPJEU02
13	25	100.0	219	6	CQ149621
14	25	100.0	219	6	CQ308221 Sequence
15	25	100.0	219	6	CQ345026 Sequence
16	25	100.0	463	6	CQ097020 Sequence
17	25	100.0	463	6	CQ135831 Sequence
18	25	100.0	463	6	CQ219128 Sequence
19	25	100.0	463	6	CQ294934 Sequence

20	25	100.0	463	6	CQ31579	CQ31579 Sequence
21	25	100.0	473	6	CQ136561	CQ136561 Sequence
22	25	100.0	473	6	CQ295678	CQ295678 Sequence
23	25	100.0	473	6	CQ312256	CQ312256 Sequence
24	25	100.0	807	6	I08556	I08556 Sequence 1
25	25	100.0	807	6	AR363343	AR363343 Sequence
26	25	100.0	966	9	HUMMDR1A07	MM29428 Human P-gly
27	25	100.0	3840	6	AX481416	AX481416 Sequence
28	25	100.0	3843	6	BD171402	BD171402 Method fo
29	25	100.0	3852	9	AF537133	AF537133 Macaca mu
30	25	100.0	3852	9	AF537134	AF537134 Macaca fa
31	25	100.0	3852	9	AY582534	AY582534 Macaca mu
32	25	100.0	3860	6	AX322787	AX322787 Sequence
33	25	100.0	3860	6	AX322789	AX322789 Sequence
34	25	100.0	3988	6	BD190394	BD190394 Phosphati
35	25	100.0	3988	6	AR452556	AR452556 Sequence
36	25	100.0	3988	6	AR024454	AR024454 Sequence
37	25	100.0	4186	6	AR399194	AR399194 Sequence
38	25	100.0	4186	6	AX108654	AX108654 Sequence
39	25	100.0	4192	9	AF016535	AF016535 Homo sapi
40	25	100.0	4195	6	AR399195	AR399195 Sequence
41	25	100.0	4195	6	AX108656	AX108656 Sequence
42	25	100.0	4264	6	AR051647	AR051647 Sequence
43	25	100.0	4264	6	AR051650	AR051650 Sequence
44	25	100.0	4378	6	E02326	E02326 Multidrug r
45	25	100.0	4553	6	CQ716151	CQ716151 Sequence

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LOCUS	AX504309					
DEFINITION	AX504309					
ACCESSION	AX504309.1	GI:23386127				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	1	Colgan,S.P.				
AUTHORS		Compositions and methods for treating hematologic malignancies and				
TITLE		multiple drug resistance				
JOURNAL		Patent: WO 0234291-A 12 02-MAY-2002;				
FEATURES		THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)				
source		location/Qualifiers				
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Db	1	AGCTTCACACCGGTAAATCCTA	25			
RESULT 2	AX504326/c	Sequence 29 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504326					
DEFINITION	AX504326					
ACCESSION	AX504326.1	GI:23386138				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					

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REFERENCE          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE              1
JOURNAL            Colgan, S.P.
                   Compositions and methods for creating hematologic malignancies and
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                   Patent: WO 0234291-A 29 02-MAY-2002;
                   THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
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QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 25 AGCTTCCACCAACGCTGTAATCCTA 1

RESULT 3
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LOCUS             BD160755
DEFINITION        Kit for assaying MDRI gene expression level.
ACCESSION         BD160755
VERSION           BD160755.1 GI:27866513
KEYWORDS          JP 2002153274-A/3.
SOURCE            synthetic construct
ORGANISM          other sequences; artificial sequences.
REFERENCE         1 (bases 1 to 120)
AUTHORS           Ujile, T., Hayashi, T., Kawase, M. and Ueji, F.
TITLE             Kit for assaying MDRI gene expression level
JOURNAL           Patent: JP 2002153274-A 3 28-MAY-2002;
                  KAINOS LAB INC
COMMENT           OS Artificial Sequence
                  PN JP 2002153274-A/3
                  PD 28-MAY-2002 JP 2000351224
                  PF 17-NOV-2000 JP 2000351224
                  PI TAKESHI UJILE, TSUKASA HAYASHI, MASAKO KAWASE, FUMIYAKI UEJI PC
                  CC C12N15/09, C12Q1/68, C12N15/00
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QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
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RESULT 4
BD160756          120 bp   DNA   linear   PAT 17-JAN-2003
LOCUS             BD160756
DEFINITION        Kit for assaying MDRI gene expression level.
ACCESSION         BD160756
VERSION           BD160756.1 GI:27866514
KEYWORDS          JP 2002153274-A/4.
SOURCE            synthetic construct

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ORGANISM          synthetic construct
                  other sequences; artificial sequences.
REFERENCE          1 (bases 1 to 120)
AUTHORS           Ujile, T., Hayashi, T., Kawase, M. and Ueji, F.
TITLE             Kit for assaying MDRI gene expression level
JOURNAL           Patent: JP 2002153274-A 4 28-MAY-2002;
                  KAINOS LAB INC
COMMENT           OS Artificial Sequence
                  PN JP 2002153274-A/4
                  PD 28-MAY-2002
                  PF 17-NOV-2000 JP 2000351224
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Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 42 AGCTTCCACCAACGCTGTAATCCTA 66

RESULT 5
CQ110210          172 bp   DNA   linear   PAT 21-JAN-2004
LOCUS             CQ110210
DEFINITION        Sequence 19069 from Patent WO0157272.
ACCESSION         CQ110210
VERSION           CQ110210.1 GI:41079573
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE         1
AUTHORS           Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE             Human genome-derived single exon nucleic acid probes useful for
                  analysis of gene expression in human placenta
JOURNAL           Patent: WO 0157272-A 19069 09-AUG-2001;
                  Aeomica, Inc. (US)
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                   EVALU4 2.30e+00"
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Query Match       100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 62 AGCTTCCACCAACGCTGTAATCCTA 86

RESULT 6
CQ148922          172 bp   DNA   linear   PAT 21-JAN-2004
LOCUS             CQ148922

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DEFINITION Sequence 16944 from Patent WO0157276.  
 ACCESSION CQ148922  
 VERSION CQ148922.1 GI:41156272  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow  
 JOURNAL Patent: WO 0157276-A 18944 09-AUG-2001;  
 Neomica, Inc. (US)

FEATURES  
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 Db 62 AGCTTCCACCACTGTAAATCCTA 86

RESULT 7  
 CQ232195 172 bp DNA linear PAT 21-JAN-2004  
 DEFINITION Sequence 19034 from Patent WO0157273.  
 ACCESSION CQ232195  
 VERSION CQ232195.1 GI:41215413  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine  
 Patent: WO 0157273-A 19034 09-AUG-2001;  
 Aeomica, Inc. (US)

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 Db 62 AGCTTCCACCACTGTAAATCCTA 86

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 DEFINITION Sequence 16613 from Patent WO0186003.  
 ACCESSION CQ307508  
 VERSION CQ307508.1 GI:41268085  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung  
 JOURNAL Patent: WO 0186003-A 18613 15-NOV-2001;  
 Neomica, Inc. (US)

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 DEFINITION Sequence 18468 from Patent WO0157275.  
 ACCESSION CQ344374  
 VERSION CQ344374.1 GI:41293445  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain  
 JOURNAL Patent: WO 0157275-A 18468 09-AUG-2001;  
 Aeomica, Inc. (US)

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DEFINITION CQ345026  
ACCESSION CQ345026.1 GI:41294097  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157275-A 19643 09-AUG-2001;  
Aeomica, Inc. (US)

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ACCESSION CQ308221.1 GI:41268798  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human lung  
JOURNAL Patent: WO 0186003-A 19326 15-NOV-2001;  
Aeomica, Inc. (US)

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LOCUS Sequence 19120 from Patent WO0157275.  
DEFINITION CQ345026  
ACCESSION CQ345026.1 GI:41294097  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human brain  
JOURNAL Patent: WO 0157275-A 19120 09-AUG-2001;  
Aeomica, Inc. (US)

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OM nucleic - nucleic search, using SW model

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## SUMMARIES

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C 4	25	100.0	4186 4 US-09-672-810-1	Sequence 1, Appli
C 5	25	100.0	4195 4 US-09-672-810-3	Sequence 3, Appli
C 6	25	100.0	4264 2 US-08-784-649A-1	Sequence 1, Appli
C 7	25	100.0	4264 2 US-08-784-649A-5	Sequence 5, Appli
C 8	25	100.0	4646 1 US-08-181-471-2	Sequence 2, Appli
C 9	25	100.0	4646 1 US-09-023-655-1167	Sequence 1167, Ap
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C 12	25	100.0	4669 3 US-09-316-167-1	Sequence 1, Appli
C 13	25	100.0	4669 4 US-09-397-233-1	Sequence 1, Appli
C 14	25	100.0	4669 6 5206352-3	Patent No. 5206352
C 15	25	100.0	4669 6 5206352-3	Patent No. 5206352
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C 18	25	100.0	8630 4 US-09-306-417-2	Sequence 2, Appli
C 19	25	100.0	9318 2 US-08-793-610-6	Sequence 6, Appli
C 20	25	100.0	9318 2 US-09-120-511-1	Sequence 1, Appli
C 21	21.8	87.2	4233 3 US-09-450-105-1	Sequence 1, Appli
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C 23	21.8	87.2	4279 4 US-09-672-725C-2	Sequence 2, Appli
C 24	21.8	87.2	4279 4 US-09-672-725C-24	Sequence 24, Appli
C 25	21.8	87.2	4279 4 US-09-672-725C-26	Sequence 26, Appli
C 26	20.2	80.8	4317 4 US-09-672-725C-3	Sequence 3, Appli
C 27	20.2	80.8	4317 4 US-10-044-671-1	Sequence 1, Appli

C 28	17	68.0	510 4 US-09-621-976-17209	Sequence 17209, A
C 29	16.6	66.4	601 4 US-09-949-016-71318	Sequence 71318, A
C 30	16.6	66.4	601 4 US-09-949-016-86805	Sequence 86805, A
C 31	16.6	66.4	601 4 US-09-949-016-179555	Sequence 179555, A
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C 37	16.6	66.4	57936 4 US-09-949-016-17533	Sequence 17533, A
C 38	16.6	66.4	128723 4 US-09-949-016-17533	Sequence 17533, A
C 39	16.6	66.4	152132 4 US-09-949-016-13845	Sequence 13845, A
C 40	16.6	66.4	152145 4 US-09-949-016-12371	Sequence 12371, A
C 41	16.6	66.4	247781 4 US-09-949-016-14193	Sequence 14193, A
C 42	16.4	65.6	694 4 US-09-270-767-2120	Sequence 2120, Ap
C 43	16.4	65.6	694 4 US-09-270-767-2120	Sequence 17402, A
C 44	16.2	64.8	601 4 US-09-949-016-30005	Sequence 30005, A
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## ALIGNMENTS

RESULT 1  
5206352-1/c  
; Patent No. 5206352  
; Applicant: Robinson, Igor B.; Paetan Ira H.; Gottesman, Michael M.  
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/622, 836  
; FILING DATE: 24-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 892,575  
; FILING DATE: 01-AUG-1986  
; APPLICATION NUMBER: 845,610  
; FILING DATE: 28-MAR-1986  
; SEQ ID NO:1:  
; LENGTH: 807  
5206352-1

Query Match 100.0%; Score 25; DB 6; Length 807;  
Best Local Similarity 100.0%; Pred. No. 0.0074; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;

QY 1 AGCTTCCACACGCTGAATCCTA 25  
DB 763 AGCTTCCACACGCTGAATCCTA 739

RESULT 2  
5206352-1/c  
; Patent No. 5206352  
; Applicant: Robinson, Igor B.; Paetan Ira H.; Gottesman, Michael M.  
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/622, 836  
; FILING DATE: 24-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 892,575  
; FILING DATE: 01-AUG-1986  
; APPLICATION NUMBER: 845,610  
; FILING DATE: 28-MAR-1986  
; SEQ ID NO:1:  
; LENGTH: 807  
5206352-1

Query Match 100.0%; Score 25; DB 6; Length 807;

Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGAATCCTA 25  
Db 763 AGCTTCAACCAACGCTGAATCCTA 739

## RESULT 3

US-09-762-195-1/c  
; Sequence 1, Application US/09762195  
; Patent No. 6677319  
; GENERAL INFORMATION:  
; APPLICANT: Stemmel, Wolfgang  
; TITLE OF INVENTION: Phosphatidylcholine as Medication with  
; FILE REFERENCE: 34691/208520  
; CURRENT APPLICATION NUMBER: US/09/762,195  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: PCT/EP9702426  
; PRIOR FILING DATE: 1999-08-06  
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3988  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-762-195-1

Query Match 100.0%; Score 25; DB 4; Length 3988;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGAATCCTA 25  
Db 710 AGCTTCAACCAACGCTGAATCCTA 686

RESULT 4  
US-09-672-810-1/c  
; Sequence 1, Application US/09672810  
; Patent No. 6617450  
; GENERAL INFORMATION:  
; APPLICANT: STOCKER, PENNY J.  
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.  
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
; FILE REFERENCE: G0307/7018  
; CURRENT APPLICATION NUMBER: US/09/672,810  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/156,921  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/158,818  
; PRIOR FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4186  
; TYPE: DNA  
; ORGANISM: Macaca fascicularis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (100)...(3940)  
US-09-672-810-1

Query Match 100.0%; Score 25; DB 4; Length 4186;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGAATCCTA 25  
Db 740 AGCTTCAACCAACGCTGAATCCTA 716

RESULT 5  
US-09-672-810-3/c  
; Sequence 3, Application US/09672810  
; Patent No. 6617450  
; GENERAL INFORMATION:  
; APPLICANT: STOCKER, PENNY J.  
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.  
; APPLICANT: CRESPI, CHARLES L.  
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
; FILE REFERENCE: G0307/7018  
; CURRENT APPLICATION NUMBER: US/09/672,810  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/156,921  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/158,818  
; PRIOR FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 4195  
; TYPE: DNA  
; ORGANISM: Macaca fascicularis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (100)...(3949)  
US-09-672-810-3

Query Match 100.0%; Score 25; DB 4; Length 4195;  
Best Local Similarity 100.0%; Pred. No. 0.0098;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGAATCCTA 25  
Db 749 AGCTTCAACCAACGCTGAATCCTA 725

RESULT 6  
US-08-784-649A-1/c  
; Sequence 1, Application US/08784649A  
; Patent No. 5830697  
; GENERAL INFORMATION:  
; APPLICANT: SIKIC, Branimir I  
; APPLICANT: Chen, Gang  
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fish & Richardson  
; STREET: 2200 Sand Hill Road  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,649A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sherwood, Pamela J  
; REGISTRATION NUMBER: Reg.No. 5830697 36,677  
; REFERENCE/DOCKET NUMBER: 06037/007001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4264 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-784-649A-1

Query Match 100.0%; Score 25; DB 2; Length 4264;  
 Best Local Similarity 100.0%; Pred. No. 0.0098;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACCGTGTAAATCCTA 25  
 Db 779 AGCTTCCACACCGTGTAAATCCTA 755

RESULT 7  
 US-08-784-649A-5/c  
 Sequence 5, Application US/08784649A  
 Patent No. 5830697  
 GENERAL INFORMATION:  
 APPLICANT: SIKIC, Branislav I  
 TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO  
 TITLE OF INVENTION: CYCLOSPORIN MODULATION  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 2200 Sand Hill Road  
 CITY: Menlo Park  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/784,649A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sherwood, Pamela J  
 REGISTRATION NUMBER: Reg.No. 5830697 36,677  
 REFERENCE/DOCKET NUMBER: 06037/007001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-322-5070  
 TELEFAX: 415-854-0875  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4264 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;  
 Best Local Similarity 100.0%; Pred. No. 0.0098;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACCGTGTAAATCCTA 25  
 Db 779 AGCTTCCACACCGTGTAAATCCTA 755

RESULT 8  
 US-08-181-471-2/c  
 Sequence 2, Application US/08181471

Patent No. 5641508  
 GENERAL INFORMATION:  
 APPLICANT: Li, Lingna  
 APPLICANT: Lishko, Valeryi K.  
 TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL  
 TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Thomas Fitting  
 STREET: 12526 High Bluff Drive, Suite 300  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92130

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/181,471  
 FILING DATE: 13-JAN-1994  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/041,553  
 FILING DATE: 02-APR-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: ANT0029P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-792-3680  
 TELEFAX: 619-792-8477  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4646 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 425..4267  
 US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.0099;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACCGTGTAAATCCTA 25  
 Db 1065 AGCTTCCACACCGTGTAAATCCTA 1041

RESULT 9  
 US-09-023-655-1167/c  
 Sequence 1167, Application US/09023655  
 Patent No. 6607879  
 GENERAL INFORMATION:  
 APPLICANT: Cocks, Benjamin G.  
 APPLICANT: Susan G. Stuart  
 APPLICANT: Jeffrey J. Seilhamer  
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 TITLE OF INVENTION: EXPRESSION  
 NUMBER OF SEQUENCES: 1508  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023.655  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4646 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g187468  
US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGGTGAATCCTA 25  
DB 1065 AGCTTCACACCGGTGAATCCTA 1041

RESULT 10  
US-08-583-276-18/c  
Sequence 18, Application US/08583276  
Patent No. 5837536  
GENERAL INFORMATION:  
APPLICANT: McDonagh, Kevin T.  
APPLICANT: Nienhuis, Arthur  
APPLICANT: Tolstoshev, Paul  
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DM4.V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,276  
FILING DATE: 05-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/332,444  
FILING DATE: 31-OCT-1994

APPLICATION NUMBER: 07/887,712  
FILING DATE: 22-MAY-1992  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 bases  
TYPE: nucleic acid  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: Genomic DNA  
US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGGTGAATCCTA 25  
DB 1065 AGCTTCACACCGGTGAATCCTA 1041

RESULT 11  
US-08-752-447-1/c  
Sequence 1, Application US/08752447  
Patent No. 5994088  
GENERAL INFORMATION:  
APPLICANT: Mechetner, Eugene  
APPLICANT: Robinson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,447  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5994088nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-9808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;

Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGCTTCAACCAAGCTGTAAATCCTA 25  
Db 1065 AGCTTCAACCAAGCTGTAAATCCTA 1041

RESULT 12  
US-09-316-167-1/c  
Sequence 1, Application US/09316167  
Patent No. 635357  
GENERAL INFORMATION:  
APPLICANT: Mechelner, Eugene  
APPLICANT: Roninson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/316.167  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752.447  
FILING DATE: 15-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6365357nan, Kevin E  
REGISTRATION NUMBER: 35.303  
REFERENCE/DOCKET NUMBER: 95.1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-9808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAAGCTGTAAATCCTA 25  
Db 1065 AGCTTCAACCAAGCTGTAAATCCTA 1041

RESULT 13  
US-09-397-233-1/c

Sequence 1, Application US/09397233  
Patent No. 6630327  
GENERAL INFORMATION:  
APPLICANT: Mechelner, Eugene  
APPLICANT: Roninson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/397.233  
FILING DATE: 16-Sep-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6630327nan, Kevin E  
REGISTRATION NUMBER: 35.303  
REFERENCE/DOCKET NUMBER: 95.1121-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-397-233-1

Query Match 100.0%; Score 25; DB 4; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAAGCTGTAAATCCTA 25  
Db 1065 AGCTTCAACCAAGCTGTAAATCCTA 1041

RESULT 14  
5206352-3/c  
Patent No. 5206352  
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,  
Michael M.  
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/622.836  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 892.575  
FILING DATE: 01-AUG-1986

; APPLICATION NUMBER: 845,610  
; FILING DATE: 28-MAR-1986  
; SEQ ID NO:3  
; LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCAACCAAGCTGTAATCCTA 25  
|||  
Db 1065 AGCTTCAACCAAGCTGTAATCCTA 1041

RESULT 15  
5206352-3/C  
; Patent No. 5206352  
; APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,  
; Michael M.  
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/622,836  
; FILING DATE: 24-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 892,575  
; FILING DATE: 01-AUG-1986  
; APPLICATION NUMBER: 845,610  
; FILING DATE: 28-MAR-1986  
; SEQ ID NO:3  
; LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCAACCAAGCTGTAATCCTA 25  
|||  
Db 1065 AGCTTCAACCAAGCTGTAATCCTA 1041

Search completed: February 9, 2005, 17:11:17  
Job time: 79.592 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds  
(without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-12

Perfect score: 1 agcttcaaccacgtgaatccta 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA: \*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
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13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	172	9	US-09-864-761-27462
2	25	100.0	209	15	US-10-101-510-284
3	25	100.0	219	9	US-09-864-761-27770
4	25	100.0	463	9	US-09-864-761-10820
5	25	100.0	473	9	US-09-864-761-11142
6	25	100.0	2307	9	US-09-805-020-31
7	25	100.0	3840	18	US-10-384-339C-30
8	25	100.0	3852	15	US-10-101-433A-1
9	25	100.0	3860	9	US-09-866-866A-1
10	25	100.0	3860	9	US-09-866-866A-3
11	25	100.0	4186	17	US-10-619-359A-1

12	25	100.0	4195	17	US-10-619-359A-3	Sequence 3, Appli
13	25	100.0	4533	9	US-09-805-020-30	Sequence 30, Appli
14	25	100.0	4643	13	US-10-072-621-2	Sequence 2, Appli
15	25	100.0	4643	14	US-10-097-340-1	Sequence 1, Appli
16	25	100.0	4643	15	US-10-007-926A-258	Sequence 258, App
17	25	100.0	4646	11	US-09-968-007A-459	Sequence 459, App
18	25	100.0	4646	11	US-09-968-007A-459	Sequence 747, App
19	25	100.0	4646	17	US-10-641-643-1167	Sequence 1167, Ap
20	25	100.0	4646	17	US-10-343-657-1	Sequence 1, Appli
21	25	100.0	4646	18	US-10-775-169-198	Sequence 198, App
22	25	100.0	4669	18	US-10-680-516-1	Sequence 1, Appli
23	25	100.0	4669	9	US-09-306-417-1	Sequence 1, Appli
24	25	100.0	8630	9	US-09-306-417-2	Sequence 2, Appli
25	21.8	87.2	4189	9	US-09-866-866A-5	Sequence 5, Appli
26	21.8	87.2	4254	17	US-10-388-934-265	Sequence 1424, Ap
27	21.8	87.2	4254	17	US-10-388-934-265	Sequence 265, App
28	21.8	87.2	4254	17	US-10-152-319A-1484	Sequence 1484, Ap
29	21.8	87.2	4298	18	US-10-335-053-32	Sequence 32, Appli
30	21.8	87.2	4788	9	US-09-866-866A-7	Sequence 7, Appli
31	20.2	80.8	2498	18	US-10-739-930-4420	Sequence 4420, Ap
32	20.2	80.8	4317	13	US-10-044-671-1	Sequence 1, Appli
33	20.2	80.8	4317	18	US-10-896-434-1	Sequence 1, Appli
34	20.2	80.8	4359	9	US-09-769-097-3	Sequence 3, Appli
35	20.2	80.8	4425	9	US-10-087-192-355	Sequence 355, App
36	19.2	76.8	71251	13	US-10-087-192-355	Sequence 40, Appl
37	18.6	74.4	44377	17	US-10-085-117-40	Sequence 160, Appl
38	18.6	74.4	94720	17	US-10-052-482-160	Sequence 2953, Ap
39	18.2	72.8	325	18	US-10-425-115-2953	Sequence 445, App
40	18.2	72.8	22644	13	US-10-087-192-445	Sequence 445, App
41	17.8	71.2	950	18	US-10-425-821-36	Sequence 26719, A
42	17.6	70.4	451	17	US-10-424-599-26719	Sequence 26719, A
43	17.6	70.4	1792	17	US-10-424-599-26721	Sequence 994, App
44	17.6	70.4	50002	13	US-10-087-192-994	Sequence 1165, Ap
45	17.6	70.4	100534	13	US-10-087-192-1165	

## ALIGNMENTS

RESULT 1  
US-09-864-761-27462  
Sequence 27462, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aesomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864, 761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27462
; LENGTH: 172
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005068.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64
; OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 3.00e-27
; OTHER INFORMATION: NT HIT: AF016535.1, EVALUE 2.00e-92
; OTHER INFORMATION: EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00
US-09-864-761-27462
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Query Match      100.0%; Score 25; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AGCTCCAACCAACGCTGTAATCCCTA 25
DB      62 AGCTCCAACCAACGCTGTAATCCCTA 86
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RESULT 2
US-10-101-510-284/c
; Sequence 284, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 284
; LENGTH: 209
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-284
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Query Match      100.0%; Score 25; DB 15; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AGCTCCAACCAACGCTGTAATCCCTA 25
DB      204 AGCTCCAACCAACGCTGTAATCCCTA 180
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RESULT 3
US-09-864-761-27770/c
; Sequence 27770, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27770
; LENGTH: 219
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: MAP TO AC002457.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
; OTHER INFORMATION: NT HIT: M29428.1, EVALUE 1.00e-120
; OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 2.00e-27
US-09-864-761-27770
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Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AGCTCCAACCAACGCTGTAATCCCTA 25
DB      143 AGCTCCAACCAACGCTGTAATCCCTA 119
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RESULT 4  
US-09-864-761-10820  
Sequence 10820, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecmca-X-1  
CURRENT FILING DATE: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 10820  
LENGTH: 463  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005068.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64  
US-09-864-761-10820

Query Match 100.0%; Score 25; DB 9; Length 463;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25  
Db 340 AGCTTCAACCAACGCTGTAATCCTA 364

RESULT 5  
US-09-864-761-11142/c  
Sequence 11142, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecmca-X-1  
CURRENT FILING DATE: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
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PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 11142  
LENGTH: 473  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC002457.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57  
US-09-864-761-11142

Query Match 100.0%; Score 25; DB 9; Length 473;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25  
Db 404 AGCTTCAACCAACGCTGTAATCCTA 380

RESULT 6  
US-09-805-020-31/c  
; Sequence 31, Application US/09805020  
; Publication No. US20020085384A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, Zuric  
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES  
; FILE REFERENCE: 2786-016AP  
; CURRENT APPLICATION NUMBER: US/09/805.020  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(2307)  
; OTHER INFORMATION: any n = a,c,g,t any unknown or other  
US-09-805-020-31

Query Match 100.0%; Score 25; DB 9; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 0.062;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCACACGCGTGAATCCTA 25  
DB 1065 AGCTTCACACGCGTGAATCCTA 1041

RESULT 7  
US-10-384-339C-30/c  
; Sequence 30, Application US/10384339C  
; Publication No. US20040175703A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreutzler, Roland  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE  
; FILE REFERENCE: 20200/2002  
; CURRENT APPLICATION NUMBER: US/10/384.339C  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: DE 10100586.5  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: DE 10155280.7  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: DE 10158411.3  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: DE 10160151.4  
; PRIOR FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 3840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; TITLE: mdt-1  
; PATENT DOCUMENT NUMBER: APO16535  
US-10-384-339C-30

Query Match 100.0%; Score 25; DB 18; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCACACGCGTGAATCCTA 25  
DB 641 AGCTTCACACGCGTGAATCCTA 617

RESULT 8

US-10-101-433A-1/c  
; Sequence 1, Application US/10101433A  
; Publication No. US20030119726A1  
; GENERAL INFORMATION:  
; APPLICANT: Hansecom, Sara  
; APPLICANT: Crespi, Charles  
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
; FILE REFERENCE: G00307/70019  
; CURRENT APPLICATION NUMBER: US/10/101.433A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: US 60/277.095  
; PRIOR FILING DATE: 2001-03-19  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1  
; LENGTH: 3852  
; TYPE: DNA  
; ORGANISM: Macaca mulatta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3852)  
US-10-101-433A-1

Query Match 100.0%; Score 25; DB 15; Length 3852;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCACACGCGTGAATCCTA 25  
DB 650 AGCTTCACACGCGTGAATCCTA 626

RESULT 9  
US-09-866-866A-1/c  
; Sequence 1, Application US/09866866A  
; Patent No. US20020102244A1  
; GENERAL INFORMATION:  
; APPLICANT: Sorrentino, Brian  
; APPLICANT: Schuetz, John  
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
; FILE REFERENCE: 1340-1-02CIR2  
; CURRENT APPLICATION NUMBER: US/09/866.866A  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 09/584,586  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: PCT/US99/11825  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: 60/086,988  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1  
; LENGTH: 3860  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCACACGCGTGAATCCTA 25  
DB 641 AGCTTCACACGCGTGAATCCTA 617

RESULT 10  
US-09-866-866A-3/c  
; Sequence 3, Application US/09866866A  
; Patent No. US20020102244A1  
; GENERAL INFORMATION:  
; APPLICANT: Sorrentino, Brian  
; APPLICANT: Schuetz, John

; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
 ; FILE REFERENCE: 1340-1-021CIP2  
 ; CURRENT APPLICATION NUMBER: US/09/866,866A  
 ; PRIOR FILING DATE: 2001-08-30  
 ; PRIOR APPLICATION NUMBER: 09/584,586  
 ; PRIOR FILING DATE: 2000-05-31  
 ; PRIOR APPLICATION NUMBER: PCT/US99/11825  
 ; PRIOR FILING DATE: 1999-05-27  
 ; PRIOR APPLICATION NUMBER: 60/086,988  
 ; PRIOR FILING DATE: 1998-05-28  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 3860  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-866-866A-3

Query Match 100.0%; Score 25; DB 9; Length 3860;  
 Best Local Similarity 100.0%; Pred. No. 0.068;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCAACCAACGCTGTAATCCTA 25  
 DB 641 AGCTTCAACCAACGCTGTAATCCTA 617

RESULT 11  
 ; US-10-619-359A-1/c  
 ; Sequence 1, Application US/10619359A  
 ; Publication No. US20040077000A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STOCKER, PENNY J.  
 ; APPLICANT: STEIMEL-CRESPI, DOROTHY T.  
 ; APPLICANT: CRESPI, CHARLES L.  
 ; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
 ; FILE REFERENCE: G00307,70020.US  
 ; CURRENT APPLICATION NUMBER: US/10/619,359A  
 ; CURRENT FILING DATE: 2003-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/156,921  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/158,818  
 ; PRIOR FILING DATE: 1999-10-12  
 ; PRIOR APPLICATION NUMBER: US 09/672,810  
 ; PRIOR FILING DATE: 2000-09-28  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4186  
 ; TYPE: DNA  
 ; ORGANISM: Macaca fascicularis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (100)...(3940)  
 ; US-10-619-359A-1

Query Match 100.0%; Score 25; DB 17; Length 4186;  
 Best Local Similarity 100.0%; Pred. No. 0.069;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCAACCAACGCTGTAATCCTA 25  
 DB 740 AGCTTCAACCAACGCTGTAATCCTA 716

RESULT 12  
 ; US-10-619-359A-3/c  
 ; Sequence 3, Application US/10619359A  
 ; Publication No. US20040077000A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STOCKER, PENNY J.  
 ; APPLICANT: STEIMEL-CRESPI, DOROTHY T.  
 ; APPLICANT: CRESPI, CHARLES L.

; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
 ; FILE REFERENCE: G00307,70020.US  
 ; CURRENT APPLICATION NUMBER: US/10/619,359A  
 ; PRIOR FILING DATE: 2003-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/156,921  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/158,818  
 ; PRIOR FILING DATE: 1999-10-12  
 ; PRIOR APPLICATION NUMBER: US 09/672,810  
 ; PRIOR FILING DATE: 2000-09-28  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 4195  
 ; TYPE: DNA  
 ; ORGANISM: Macaca fascicularis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (100)...(3949)  
 ; US-10-619-359A-3

Query Match 100.0%; Score 25; DB 17; Length 4195;  
 Best Local Similarity 100.0%; Pred. No. 0.069;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCAACCAACGCTGTAATCCTA 25  
 DB 749 AGCTTCAACCAACGCTGTAATCCTA 725

RESULT 13  
 ; US-09-805-020-30/c  
 ; Sequence 30, Application US/09805020  
 ; Publication No. US20020086384A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEVINE, ZURIT  
 ; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES  
 ; FILE REFERENCE: 2786-0168P  
 ; CURRENT APPLICATION NUMBER: US/09/805,020  
 ; CURRENT FILING DATE: 2001-03-13  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 30  
 ; LENGTH: 4533  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)...(4533)  
 ; OTHER INFORMATION: any n = a,c,g,t any unknown or other  
 ; US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCAACCAACGCTGTAATCCTA 25  
 DB 1065 AGCTTCAACCAACGCTGTAATCCTA 1041

RESULT 14  
 ; US-10-072-621-2/c  
 ; Sequence 2, Application US/10072621  
 ; Publication No. US20020169137A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reiner, Peter B.  
 ; APPLICANT: Connop, Bruce P.  
 ; APPLICANT: Pollard, Michelle  
 ; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION  
 ; FILE REFERENCE: 100103.402  
 ; CURRENT APPLICATION NUMBER: US/10/072,621

;; CURRENT FILING DATE: 2002-02-08  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 4643  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACACGCTGAATCCTA 25  
DB 1065 AGCTTCCACACGCTGAATCCTA 1041

RESULT 15  
US-10-097-340-1/c  
; Sequence 1, Application US/10097340  
; Publication No. US20030087250A1  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNANVARAPU  
; APPLICANT: Sebastian HOERSCH  
; APPLICANT: Shubhangi KAWATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS  
; APPLICANT: Michael MORRISSEY  
; APPLICANT: Peter OLANDT  
; APPLICANT: Ami SEN  
; APPLICANT: Peter VEIBY  
; APPLICANT: Gordon B. MILLS  
; APPLICANT: Robert C. BAST, Jr.  
; APPLICANT: Karen LU  
; APPLICANT: Rosemarie SCHMANDT  
; APPLICANT: Xumei ZHAO  
; APPLICANT: Karen GLATT  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; FILE REFERENCE: MRI-030  
; CURRENT APPLICATION NUMBER: US/10/097,340  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 4643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-097-340-1

Query Match 100.0%; Score 25; DB 14; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACACGCTGAATCCTA 25  
DB 1065 AGCTTCCACACGCTGAATCCTA 1041



PS Example 2; Page 12; 92pp; English.

XX The invention relates to a method of treating a subject having or at risk

CC of developing a haematologic malignancy or multidrug resistance (MDR).

CC The method involves administering hypoxia inducible factor-1 (HIF-1)

CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding

CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive

CC element (HRE) binding molecules or antisense nucleic acid molecules and

CC SUMO-1 binding molecules or antisense molecules are useful for treating a

CC subject having or at risk of developing haematologic malignancy or MDR

CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders

CC include lymphocytic leukaemia or chronic lymphoproliferative disorders

CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid

CC disorders include chronic or acute myeloid leukaemia, e.g. angio-genic

CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The

CC invention is used in gene therapy. The present sequence is human mdr1

CC gene HIF-1 binding site DNA

XX

SQ Sequence 25 BP; 6 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACCGGTGAATCCTA 25

DB 25 AGCTTCCAAACCGGTGAATCCTA 1

RESULT 2

AAD39001 standard; DNA; 25 BP.

AC AAD39001;

XX 23-SEP-2002 (first entry)

XX Human mdr1-HRE antisense oligonucleotide #4.

XX

KM Human haematologic malignancy; multidrug resistance; MDR; SUMO-1;

KM hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;

KM lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;

KM myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;

KM angio-genic myeloid metaplasia; myeloid leukaemia; gene therapy;

KM polycythaemia vera; hypoxia responsive element; HRE; antisense;

KM phosphorothioate backbone; ss.

XX

OS Homo sapiens.

OS Synthetic.

OS

PH Key Location/Qualifiers

FT modified\_base 1..25

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

XX WO200234291-A2.

XX

PD 02-MAY-2002.

XX

XX 25-OCT-2001; 2001WO-US049856.

XX

XX 26-OCT-2000; 2000US-0243542P.

XX

XX (BGM ) BRIGHAM & WOMENS HOSPITAL INC.

XX

XX Colgan SP;

XX

XX WPI; 2002-471427/50.

XX

XX Treating a subject (at risk of) having a haematologic malignancy or

PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT binding molecules.

XX

XX Claim 14; Page 43; 92pp; English.

XX

CC The invention relates to a method of treating a subject having or at risk

CC of developing a haematologic malignancy or multidrug resistance (MDR).

CC The method involves administering hypoxia inducible factor-1 (HIF-1)

CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding

CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive

CC element (HRE) binding molecules or antisense nucleic acid molecules and

CC SUMO-1 binding molecules or antisense molecules are useful for treating a

CC subject having or at risk of developing haematologic malignancy or MDR

CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders

CC include lymphocytic leukaemia or chronic lymphoproliferative disorders

CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid

CC disorders include chronic or acute myeloid leukaemia, e.g. angio-genic

CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The

CC invention is used in gene therapy. The present sequence is an antisense

CC oligo targeted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its

CC expression. This oligo is used in the exemplification of the invention

XX

SQ Sequence 25 BP; 8 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACCGGTGAATCCTA 25

DB 1 AGCTTCCAAACCGGTGAATCCTA 25

RESULT 3

ABK87742/c

ID ABK87742 standard; DNA; 120 BP.

XX

XX ABK87742;

XX

DT 07-OCT-2002 (first entry)

XX

XX Multiple drug resistance gene, MDR1, sequence #3.

DS

XX MDR1; dr; multiple drug resistance gene; nucleic acid amplification;

KM MDR1 expression level; multiple drug resistance.

KM

XX Unidentified.

OS

XX JP2002153274-A.

PN

XX 28-MAY-2002.

XX

PD 17-NOV-2000; 2000JP-00351224.

XX

XX 17-NOV-2000; 2000JP-00351224.

PR

XX (KAIN-) KAINOSU KK.

PA

XX WPI; 2002-552738/59.

XX

XX A primer for amplifying a nucleic acid comprises a specific

PT oligonucleotide sequence for determination of Multiple Drug Resistance

PT gene expression level by nucleic acid amplification.

PT

XX Claim 7; Page 6; 7pp; Japanese.

XX

XX The invention relates to a primer for amplifying a nucleic acid

CC comprising a 15 to 30 base continuous oligonucleotides of an MDR1

CC (multiple drug resistance gene 1) gene fragment appearing as ABK87740.

CC Also included are a kit for quantitatively determining the expression

CC level of MDR1 gene, a probe for capturing a nucleic acid, a reagent for

CC amplifying a nucleic acid and diagnosis of the drug resistance of a

CC patient. The primer is useful for the determination of MDR expression

CC level by nucleic acid amplification. The present sequence is a fragment



CC of the MDR1 gene  
 XX Sequence 120 BP; 28 A; 21 C; 27 G; 44 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 25; DB 6; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 0.03;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACGCTGTAAATCCTA 25  
 |||||  
 DB 79 AGCTTCCACACGCTGTAAATCCTA 55

RESULT 4  
 ABK87743  
 ID ABK87743 standard; DNA; 120 BP.  
 AC ABK87743;  
 XX  
 XX 07-OCT-2002 (first entry)  
 DT  
 XX  
 DE Multiple drug resistance gene, MDR1, sequence #4.  
 XX  
 KM MDR1; drug, multiple drug resistance gene; nucleic acid amplification;  
 KM MDR1 expression level; multiple drug resistance.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2002153274-A.  
 PD  
 PD 28-MAY-2002.  
 XX  
 PF 17-NOV-2000; 2000JP-00351224.  
 XX  
 PR 17-NOV-2000; 2000JP-00351224.  
 XX  
 PA (KAIN-) KAINOSU KK.  
 XX  
 XX WPI; 2002-552736/59.  
 DR  
 XX  
 PT A primer for amplifying a nucleic acid comprises a specific  
 PT oligonucleotide sequence for determination of Multiple Drug Resistance  
 PT gene expression level by nucleic acid amplification.  
 XX  
 PS Claim 9; Page 6; 7pp; Japanese.  
 XX  
 CC The invention relates to a primer for amplifying a nucleic acid  
 CC comprising a 15 to 30 base continuous oligonucleotide of an MDR1  
 CC (multiple drug resistance gene 1) gene fragment appearing as ABK87740.  
 CC Also included are a kit for quantitatively determining the expression  
 CC level of MDR1 gene, a probe for capturing a nucleic acid, a reagent for  
 CC amplifying a nucleic acid and diagnosis of the drug resistance of a  
 CC patient. The primer is useful for the determination of MDR expression  
 CC level by nucleic acid amplification. The present sequence is a fragment  
 CC of the MDR1 gene  
 CC  
 XX  
 SQ Sequence 120 BP; 44 A; 27 C; 21 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 0.03;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACGCTGTAAATCCTA 25  
 |||||  
 DB 42 AGCTTCCACACGCTGTAAATCCTA 66

RESULT 5  
 AA150383  
 ID AA150383 standard; DNA; 172 BP.  
 AC AA150383;  
 XX

DT 17-OCT-2001 (first entry)  
 XX  
 DE Probe #19069 used to measure gene expression in human placenta sample.  
 XX  
 KM Probe; microarray; human; placenta; antenatal diagnosis;  
 KM genetic disorder; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200157272-A2.  
 XX  
 PD 09-AUG-2001.  
 PD  
 PF 30-JAN-2001; 2001WO-US000663.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-0063366P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI  
 DR WPI; 2001-48897/53.  
 XX  
 XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human placenta.  
 PT  
 PS Claim 25; SEQ ID NO 19069; 654bp; English.  
 XX  
 XX The present invention relates to single exon nucleic acid probes (SENP).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders  
 CC  
 XX  
 SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACGCTGTAAATCCTA 25  
 |||||  
 DB 62 AGCTTCCACACGCTGTAAATCCTA 86

RESULT 6  
 AAK44387  
 ID AAK44387 standard; DNA; 172 BP.  
 AC AAK44387;  
 XX  
 DT 06-NOV-2001 (first entry)  
 DT  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 18944.  
 XX  
 KM Human; bone marrow expressed exon; gene expression analysis; probe;  
 KM microarray; cancer; leukemia; lymphoma; myeloma; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PM WO200157276-A2.  
 PM  
 PD 09-AUG-2001.  
 PD  
 PF 30-JAN-2001; 2001WO-US000668.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 XX

PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488900/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human bone marrow.  
 XX  
 PS Example 4; SEQ ID NO 18944; 658bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
 CC the probes of the invention  
 XX  
 SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;  
 XX  
 QY Query Match 100.0%; Score 25; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 AGCTTCCACACGCTGTAATCCTA 25  
 62 AGCTTCCACACGCTGTAATCCTA 86  
 XX  
 RESULT 7  
 AAK18477  
 ID AAK18477 standard; DNA; 172 BP.  
 XX  
 AC AAK18477;  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 DE Human brain expressed single exon probe SEQ ID NO: 18468.  
 XX  
 KW Human: brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001;  
 XX  
 PF 30-JAN-2001; 2001WO-US000667.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483446/52.  
 XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human

PT brains.  
 XX  
 PS Example 4; SEQ ID NO 18468; 650bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention  
 XX  
 SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;  
 XX  
 QY Query Match 100.0%; Score 25; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 AGCTTCCACACGCTGTAATCCTA 25  
 62 AGCTTCCACACGCTGTAATCCTA 86  
 XX  
 RESULT 8  
 ABS44044  
 ID ABS44044 standard; DNA; 172 BP.  
 XX  
 AC ABS44044;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Human liver single exon probe, SEQ ID NO 19034.  
 XX  
 KW Human: single exon nucleic acid probe; liver; cirrhosis;  
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
 KW coronary heart disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000664.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488989/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human adult liver.  
 XX  
 PS Claim 4; SEQ ID NO 19034; 658bp; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe (SENP) (1) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 1109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (1) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

CC associated with coronary heart disease, AB25011-AB851005 represent human  
CC liver single exon nucleic acid probes of the invention. Note: The  
CC sequence information for this patent does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 AGCTTCCACCACTGTAAATCCTA 25  
62 AGCTTCCACCACTGTAAATCCTA 86  
Db  
RESULT 9  
AB2518622  
ID AB2518622 standard; DNA; 172 BP.  
XX  
AC AB2518622;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 18613.  
XX  
XX Human; de; single exon probe; asthma; lung cancer; COPD; ILD;  
XX chronic obstructive pulmonary disease; interstitial lung disease;  
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;  
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;  
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
XX primary ciliary dyskinesia; pulmonary hypertension;  
XX hyaline membrane disease; open reading frame; ORF.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO200186003-A2.  
XX  
XX PD 15-NOV-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000665.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI, 2002-114183/15.  
XX  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
XX measure gene expression in human lung samples.  
XX  
XX Claim 4; SEQ ID NO 18613; 634bp; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
XX nucleic acid probes for measuring gene expression in a sample derived  
XX from human lung comprising single exon nucleic acid probes having one of  
XX 12614 nucleic acid sequences mentioned in the specification, or their  
XX complements or the 12387 open reading frames derived from the 12614  
XX probes. Also included are a microarray comprising the novel set of probes  
XX; the novel set of probes which hybridise at high stringency to a nucleic  
XX acid expressed in the human lung; measuring gene expression in a sample  
XX derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung  
CC array; and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Kartagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a single exon probe open reading frame of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 AGCTTCCACCACTGTAAATCCTA 25  
62 AGCTTCCACCACTGTAAATCCTA 86  
Db

RESULT 10  
AB235172/c  
ID AB235172 standard; cDNA; 209 BP.  
XX  
XX AC AB235172;  
XX  
XX DT 05-FEB-2003 (first entry)  
XX  
XX DE Human gene expression profile polynucleotide SEQ ID NO 284.  
XX  
XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;  
XX bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;  
XX tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;  
XX gene expression; gene; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO200274979-A2.  
XX  
XX PD 26-SEP-2002.  
XX  
XX 20-MAR-2002; 2002WO-US008456.  
XX  
XX 20-MAR-2001; 2001US-0276947P.  
XX  
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
XX  
XX Wan J, Wang Y;  
XX  
XX WPI, 2002-740862/80.  
XX  
XX New gene expression profile generated from primary, endothelial,  
XX

PT epithelial, and muscle cell types, useful for identifying disease  
 PT pathologies involving alterations of gene expression, e.g. cancer.  
 XX  
 PS Claim 10, Page 448; 850pp; English.

XX The invention relates to a gene expression profile comprising one or more  
 CC genes (AB234889-AB235692) and generated from a cell type. The cell type  
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,  
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery  
 CC endothelium, myometrium microvascular endothelium, keratinocyte  
 CC epithelium, bronchial epithelium, mammary epithelium, prostate  
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,  
 CC small airway epithelium, renal epithelium, umbilical artery smooth  
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,  
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,  
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,  
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,  
 CC osteoblasts or prostate stromal cell. The gene expression profile is used  
 CC for determining the level of RNA expression for a sample, determining the  
 CC phenotype of a cell and distinguishing cell types. The gene or a protein  
 CC expression profile is useful in identifying disease pathologies involving  
 CC alterations of gene expression. The assessment of expression profiles may  
 CC provide meaningful information with respect to tumour type and stage,  
 CC treatment methods, and prognosis. The gene or protein expression profile  
 CC may also be used for creating microarrays. The microarray is useful for  
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or  
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue  
 CC identifications and in identifying promising antibiotics, antiviral or  
 CC antifungal agents

XX Sequence 209 BP; 65 A; 39 C; 38 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 209;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACACGCTGTAATCCTA 25  
 |||||  
 DB 204 AGCTTCCACACGCTGTAATCCTA 180

RESULT 11  
 AAK45086/c  
 ID AAK45086 standard; DNA; 219 BP.

XX AAK45086;

DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 19643.

XX Human, bone marrow expressed exon; gene expression analysis; probe;  
 KM microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX MO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI

XX WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 19643; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of  
 the probes of the invention

XX Sequence 219 BP; 54 A; 38 C; 51 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 0.033;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACACGCTGTAATCCTA 25  
 |||||  
 DB 143 AGCTTCCACACGCTGTAATCCTA 119

RESULT 12  
 AAK19129/c  
 ID AAK19129 standard; DNA; 219 BP.

XX AAK19129;

DT 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe SEQ ID NO: 19120.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
 XX ss.

XX Homo sapiens.

XX MO200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000667.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains.

XX Example 4; SEQ ID NO 19120; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention  
 XX sequence 219 BP, 54 A, 38 C, 51 G, 76 T, 0 U, 0 Other;  
 SQ

Query Match  
 Best Local Similarity 100.0%; Score 25; DB 4; Length 219;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACCGTGAATCCTA 25  
 Db 143 AGCTTCCACACCGTGAATCCTA 119

RESULT 13  
 ABS19335/C  
 ID ABS19335 standard; DNA, 219 BP.  
 XX  
 AC ABS19335;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 19326.  
 KW Human; der; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease; open reading frame; ORF.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180332P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-11483/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 measure gene expression in human lung samples.  
 XX  
 PS Claim 4; SEQ ID NO 19326; 634bp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression with a  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarray having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX

SQ Sequence 219 BP, 54 A, 38 C, 51 G, 76 T, 0 U, 0 Other;  
 Query Match  
 Best Local Similarity 100.0%; Score 25; DB 6; Length 219;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACCGTGAATCCTA 25  
 Db 143 AGCTTCCACACCGTGAATCCTA 119

RESULT 14  
 ID AAI37193 standard; DNA, 463 BP.  
 XX  
 AC AAI37193;  
 XX  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Probe #5879 used to measure gene expression in human placenta sample.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157272-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000663.  
 XX  
 PR 04-FEB-2000; 2000US-0180332P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-48897/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.  
XX  
PS Claim 25; SEQ ID NO 5879; 654bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP).  
CC The present sequence is one such probe. The probes are useful for  
CC predicting a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders  
XX  
SQ Sequence 463 BP; 153 A; 100 C; 98 G; 112 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 4; Length 463;  
Best Local Similarity 100.0%; Pred. No. 0.036;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTTCCAACCAACGTTAAATCCTA 25  
Db 340 AGCTTCCAACCAACGTTAAATCCTA 364

## RESULT 15

AAK31296  
ID AAK31296 standard; DNA; 463 BP.

AAK31296;

06-NOV-2001 (first entry)

Human bone marrow expressed single exon probe SEQ ID NO: 5853.

Human; bone marrow expressed exon; gene expression analysis; probe;  
microarray; cancer; leukaemia; lymphoma; myeloma; ss.

Homo sapiens.

W0200157276-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000668.

04-FEB-2000; 2000US-0180312P.  
26-MAY-2000; 2000US-0207456P.  
30-JUN-2000; 2000US-00608408.  
03-AUG-2000; 2000US-00632366.  
21-SEP-2000; 2000US-0234687P.  
27-SEP-2000; 2000US-0236359P.  
04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for analyzing  
gene expression in human bone marrow.

Example 4; SEQ ID NO 5853; 658bp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid  
probes which are derived from genomic sequences expressed in the human  
bone marrow. They can be used to measure gene expression in bone marrow  
samples, which may enable the improved diagnosis and treatment of cancers  
such as lymphoma, leukemia and myeloma. The present sequence is one of  
the probes of the invention

Sequence 463 BP; 153 A; 100 C; 98 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 463;  
Best Local Similarity 100.0%; Pred. No. 0.036;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAACCAACGTTAAATCCTA 25  
Db 340 AGCTTCCAACCAACGTTAAATCCTA 364

Search completed: February 9, 2005, 16:05:58  
Job time : 247.69 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds  
(without alignments)  
388.593 Million cell updates/sec

Title: US-10-007-255-12

Perfect score: 25  
Sequence: 1 agcttccaccacgtgtaactccta 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hlc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_g881.\*  
9: gb\_g882.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	3843	9	AY408954 Homo sapi
C 2	25	100.0	3843	9	AY408955 Pan trogl
C 3	21.8	87.2	3182	3	AK030328 Mus muscu
C 4	21.8	87.2	3816	9	AY408956 Mus muscu
C 5	20.8	83.2	682	7	CP176579 805414 MA
C 6	20.2	80.8	478	2	BE217416 fbn-1094
C 7	20.2	80.8	806	3	CNSOAI14
C 8	19.8	79.2	489	3	AZ957679 2M0224F07
C 9	19.8	79.2	775	4	BI691631 603107314
C 10	19.2	76.8	526	8	BH521842 BOGOF607F
C 11	19.2	76.8	553	1	AU291400 AU291400
C 12	19.2	76.8	589	8	BH174634 B1F51B20
C 13	19.2	76.8	604	8	BH713924 BOMC138TF
C 14	19.2	76.8	617	8	BH696214 BOMNB04TR
C 15	19.2	76.8	634	8	BH698731 BOMC167TF
C 16	19.2	76.8	652	8	AZ341385 1M0073B15
C 17	19.2	76.8	656	8	CC951154 BOMM45TRF
C 18	19.2	76.8	657	8	BH983322 cdf12c02.
C 19	19.2	76.8	692	8	BZ010051 oej74907.
C 20	19.2	76.8	722	9	CC967311 BOIMH63TR
C 21	19.2	76.8	731	5	BO974293 OH15E03.
C 22	19.2	76.8	779	8	BZ427781 BONO337TR
C 23	19.2	76.8	783	8	BH480667 BOHC844TR
C 24	19.2	76.8	799	8	BH701776 BOME11TF

25	19.2	76.8	804	8	BH600441	BH600441 BOCJ274TR
26	19.2	76.8	805	8	BH068818	BH068818 RPCT-24-3
27	19.2	76.8	840	8	BZ493588	BZ493588 BOMKX20TF
C 28	19.2	76.8	865	9	CC909091	CC909091 t047p02ba
C 29	19.2	76.8	983	8	BZ501403	BZ501403 BOMK159TF
C 30	19.2	76.8	2239	3	AK090183	AK090183 Mus muscu
C 31	18.8	75.2	732	9	AG425665	AG425665 Mus muscu
C 32	18.8	75.2	1749	3	AK086811	AK086811 Mus muscu
C 33	18.6	74.4	169	9	CE015031	CE015031 tigr-g88-
C 34	18.6	74.4	173	9	CR063094	CR063094 Forward 8
C 35	18.6	74.4	201	8	AZ001999	AZ001999 RPCT-23-3
C 36	18.6	74.4	233	9	CR055056	CR055056 Forward 8
C 37	18.6	74.4	337	4	BI301745	BI301745 UI-R-DL0-
C 38	18.6	74.4	337	4	BI301966	BI301966 UI-R-DL0-
C 39	18.6	74.4	358	2	BB872680	BB872680 BB872680
C 40	18.6	74.4	389	2	BF806551	BF806551 PM2-C1005
C 41	18.6	74.4	412	2	BF805641	BF805641 PM2-C1005
C 42	18.6	74.4	412	2	BF808478	BF808478 PM2-C1005
C 43	18.6	74.4	463	8	BH858848	BH858848 S3_x011c2
C 44	18.6	74.4	504	8	BH858849	BH858849 S3_x011c2
C 45	18.6	74.4	528	1	AI965324	AI965324 fc89h05.x

#### ALIGNMENTS

RESULT 1  
AY408954/c 3843 bp DNA linear GSS 15-DEC-2003  
DEFINITION Homo sapiens ABCB1 gene, VIRUAL TRANSCRIPT, partial sequence,  
LOCUS genomic survey sequence.  
ACCESSION AY408954  
VERSION AY408954.1 GI:39764922  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3843)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 3843)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITL Direct Submission  
JOURNL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..3843  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..3843  
/gene="ABCB1"  
/locus\_tag="HCM3396"  
ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTTCAACACGCTAAATCCTA 25  
|||||

Db 641 AGCTCCACCGCGTGAATCCTA 617

RESULT 2  
AY408955/c 3843 bp DNA linear GSS 15-DEC-2003  
LOCUS Pan troglodytes ABCB1 gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY408955 GI:39764923  
VERSION GSS.  
KEYWORDS Pan troglodytes (chimpanzee)  
SOURCE Pan troglodytes  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,  
Fertler,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J.,  
Adams,M.D. and Cargill,M.  
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene tries  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS 2 (bases 1 to 3843)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,  
Fertler,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Glade Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
Location/Qualifiers  
1..3843  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
1..3843  
/gene="ABCB1"  
/locus\_tag="HCOM3396"  
ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCCACCGCGTGAATCCTA 25  
Db 641 AGCTCCACCGCGTGAATCCTA 617  
RESULT 3  
AK030328/c 3182 bp mRNA linear HTC 03-APR-2004  
LOCUS Mus musculus 11 days pregnant adult female ovary and uterus cDNA,  
DEFINITION RIKEN full-length enriched library, clone:5031438E12  
product:ATP-binding cassette, sub family B (MDR/TAP), member 1B,  
full insert sequence.  
ACCESSION AK030328  
VERSION AK030328.1 GI:26081769  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE  
AUTHORS 2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE  
AUTHORS 3  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Kono,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M.,  
Yoneda,Y., Iehikawa,T., Ozawa,K., Tanaka,T., Ohara,Y., Matsura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multichannel sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 20530913  
PUBMED 11076861  
REFERENCE  
AUTHORS 4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE  
AUTHORS 5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE  
AUTHORS 6 (bases 1 to 3182)  
Adachi,D., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
Kato,H., Kawai,D., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akaike,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toyo,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUN-2001) Yoshinide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan [E-mail: genome-res@gsf.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216]  
COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
FEATURES  
source  
Location/Qualifiers  
1..3182  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="FANTOM:DB:5031438E12"  
/db\_xref="taxon:10090"  
/clone="5031438E12"  
/sex="female"  
/tissue\_type="ovary and uterus"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="11 days pregnant adult"



msc\_feature 1. .3182  
/note="ATP-binding cassette, sub-family B (MDR/TRAP),  
member 1B (MDR1G1:97568, GB|NM\_011075, evidence: BLASTN,  
99%, match=2587)"

ORIGIN  
Query Match 87.2%; Score 21.8; DB 3; Length 3182;  
Best Local Similarity 92.0%; Pred. No. 11;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25  
Db 730 AGCTTCCACACCTTATTAATCCTA 706

RESULT 4  
LOCUS AY408956/c 3816 bp DNA linear GSS 15-DEC-2003  
DEFINITION Mus musculus ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,  
ACCESSION AY408956  
VERSION AY408956.1 GI:39764924  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Clark A.G., Glanowski S., Nielson R., Thomas P., Kejarival A.,  
Todd M.A., Tanenbaum D.M., Cavello D.R., Lu F., Murphy B.,  
Ferreira S., Wang G., Zheng X.H., White T.J., Shtinsky J.J.,  
Adams M.D. and Cargill M.  
Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene trices

TITLE Science 302 (5652), 1960-1963 (2003)  
JOURNAL 14671302  
PUBMED 2 (bases 1 to 3816)  
AUTHORS Clark A.G., Glanowski S., Nielson R., Thomas P., Kejarival A.,  
Todd M.A., Tanenbaum D.M., Cavello D.R., Lu F., Murphy B.,  
Ferreira S., Wang G., Zheng X.H., White T.J., Shtinsky J.J.,  
Adams M.D. and Cargill M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
SOURCE Location/Qualifiers  
1. .3816  
/organism="Mus musculus"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:10090"  
<1\_>3816  
/gene="ABCB1"  
/locus\_tag="HMCJ3396"

ORIGIN  
Query Match 87.2%; Score 21.8; DB 9; Length 3816;  
Best Local Similarity 92.0%; Pred. No. 11;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25  
Db 629 AGCTTCCACACGCGTAATCCTA 605

RESULT 5  
LOCUS CF176979/c 682 bp mRNA linear EST 28-JUL-2003  
DEFINITION 805414 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.  
ACCESSION CF176979  
VERSION CF176979.1 GI:33288755  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

AUTHORS 1 (bases 1 to 682)  
Smith T.P.L., Freking B.A., Ford J.J., Vallec J.L., Fox J.,  
Wise T.A., Noneman D.J., Wray J.E. and Keeler J.W.  
A second set of porcine ESTs from a pooled-tissue normalized  
library

TITLE Unpublished (2003)  
JOURNAL Contact: Smith TPL  
COMMENT USA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_all option. Vector identified with  
cross\_match v0.990329.  
Plate: SRG8002 row: F column: 24  
Seq primer: GTAATACGACTCATATAGCG.

FEATURES  
SOURCE Location/Qualifiers  
1. .682  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
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/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_id="MARC 3P1G"  
/note="Vector: pCDNA3.1; Site 1: EcoRI, Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including brain, liver, muscle, placenta/endometrium,  
ovary, testes, and bone marrow."

ORIGIN  
Query Match 83.2%; Score 20.8; DB 7; Length 682;  
Best Local Similarity 91.7%; Pred. No. 28;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCT 24  
Db 388 AGCTTCCACACCGTAATGCT 365

RESULT 6  
LOCUS BE217416/c 478 bp mRNA linear EST 03-JUL-2000  
DEFINITION fbn-1094 Cattle pUC18 library Bos taurus cDNA, mRNA sequence.  
ACCESSION BE217416  
VERSION BE217416.1 GI:8904732  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 478)  
AUTHORS Schweinin M., Dorroch U. and Goldammer T.  
TITLE Mapping of differentially expressed hepatic and intestinal EST's in  
cattle  
COMMENT Unpublished (2000)  
Contact: Schweinin M  
Molecular Biology  
FBN Dummerstorf  
2nd Wilhelm-Stahl-Allee, Dummerstorf, 18196, Germany  
Tel: 0049-038208-68700  
Fax: 0049-038208-68702  
Email: schweinin@fbn-dummerstorf.de  
High quality sequence stop: 478  
POLYA=Yes.

FEATURES  
SOURCE Location/Qualifiers  
1. .478  
/organism="Bos taurus"  
/mol\_type="mRNA"

/db\_xref="taxon:9913"  
 /sex="female"  
 /tissue\_type="intestine"  
 /dev\_stage="lactation"  
 /lab\_host="XU-blue"  
 /clone\_id="Cattle pUC18 library"  
 /note="Vector: pUC18 Sma I/BAP"

## ORIGIN

Query Match 80.8%; Score 20.2; DB 2; Length 478;  
 Best Local Similarity 86.0%; Pred. No. 54;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 AGCTTCACACGCTGTAATCCTA 25  
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 309 AGCTTCACACTTCTGTAATCCTA 285

RESULT 7  
 CDS0A1M4 806 bp mRNA linear HTC 06-FEB-2004  
 LOCUS Arabidopsis thaliana Full-length cDNA-Complete sequence from clone  
 DEFINITION GSLTIL252G04 of Siliques of strain col-0 of Arabidopsis thaliana  
 (thale cress).  
 BX832952  
 BX832952.1 GI:42459179  
 HTC; GSLT cDNA.  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 806)  
 Castelli V., Aury J.M., Jallou O., Wincker P., Clepet C.,  
 Menard M., Craud C., Querier F., Scarpelli C., Schachter V.,  
 Temple G., Caboche M., Weissenbach J. and Salanoubat M.  
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
 A Combined Approach to Evaluate and Improve Arabidopsis Genome  
 Annotation  
 Unpublished  
 2 (bases 1 to 806)  
 Genoscope.  
 Direct Submission  
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 The sequences are based on single pass reads.  
 Life Technologies (a division of Invitrogen) members carried out  
 full-length libraries construction : Temple G.  
 Genoscope members carried out sequencing and annotation : Castelli  
 V., Aury J.M., Jallou O., Wincker P., Menard M., Craud C.,  
 Schachter V., Weissenbach J., Salanoubat M.  
 URV INRA : Clepet C., Caboche M.  
 Annotation is based on the June 2003 version of the Arabidopsis  
 genome released by MIPS (Munich Information Center for Protein  
 Sequences) . 5 prime and 3 prime are assembled with Phrap.  
 http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full  
 length  
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.  
 Location/Qualifiers  
 1. 806  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /strain="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="GSLTIL252G04"  
 /tissue\_type="Siliques"  
 /plasmid="pCMVSPORT\_6"  
 1. 806  
 /gene="At5g51440"

Best Local Similarity 88.0%; Pred. No. 57;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 AGCTTCACACGCTGTAATCCTA 25  
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 371 AGCTTCACACGCTGTAATCCTA 347

## RESULT 8

AZ957679 489 bp DNA linear GSS 27-APR-2001  
 LOCUS 2M0224F07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 DEFINITION clone UUGC2M0224F07 R, genomic survey sequence.  
 AZ957679  
 AZ957679.1 GI:13828906  
 GSS.

KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 489)  
 Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamill C.,  
 Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,  
 Reilly M., Rose M., Rose R., Stokes R., Tingey A., von  
 Niederhausern A. and Wright D., Weiss R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0224 row: F column: 07  
 Seq primer: CACACGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 489.  
 Location/Qualifiers  
 1. 489  
 /organism="Mus musculus"  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0224F07"  
 /sex="Female"  
 /lab\_host="E. coli strain XU10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv, Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XU10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

## REFERENCE

1 (bases 1 to 806)  
 Castelli V., Aury J.M., Jallou O., Wincker P., Clepet C.,  
 Menard M., Craud C., Querier F., Scarpelli C., Schachter V.,  
 Temple G., Caboche M., Weissenbach J. and Salanoubat M.  
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
 A Combined Approach to Evaluate and Improve Arabidopsis Genome  
 Annotation  
 Unpublished  
 2 (bases 1 to 806)  
 Genoscope.  
 Direct Submission  
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 The sequences are based on single pass reads.  
 Life Technologies (a division of Invitrogen) members carried out  
 full-length libraries construction : Temple G.  
 Genoscope members carried out sequencing and annotation : Castelli  
 V., Aury J.M., Jallou O., Wincker P., Menard M., Craud C.,  
 Schachter V., Weissenbach J., Salanoubat M.  
 URV INRA : Clepet C., Caboche M.  
 Annotation is based on the June 2003 version of the Arabidopsis  
 genome released by MIPS (Munich Information Center for Protein  
 Sequences) . 5 prime and 3 prime are assembled with Phrap.  
 http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full  
 length  
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.  
 Location/Qualifiers  
 1. 806  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /strain="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="GSLTIL252G04"  
 /tissue\_type="Siliques"  
 /plasmid="pCMVSPORT\_6"  
 1. 806  
 /gene="At5g51440"

## JOURNAL

## AUTHORS

## COMMENT

## FEATURES

## source

1. 806  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /strain="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="GSLTIL252G04"  
 /tissue\_type="Siliques"  
 /plasmid="pCMVSPORT\_6"  
 1. 806  
 /gene="At5g51440"

## ORIGIN

Query Match 80.8%; Score 20.2; DB 3; Length 806;

## JOURNAL

## AUTHORS

1 (bases 1 to 489)  
 Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamill C.,  
 Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,  
 Reilly M., Rose M., Rose R., Stokes R., Tingey A., von  
 Niederhausern A. and Wright D., Weiss R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0224 row: F column: 07  
 Seq primer: CACACGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 489.  
 Location/Qualifiers  
 1. 489  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0224F07"  
 /sex="Female"  
 /lab\_host="E. coli strain XU10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv, Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XU10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## FEATURES

## source

1. 489  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0224F07"  
 /sex="Female"  
 /lab\_host="E. coli strain XU10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv, Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XU10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 79.2%; Score 19.8; DB 8; Length 489;

Best Local Similarity 91.3%; Pred. No. 85;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 430 AGCTTCAACACCTGTAAATCC 452

RESULT 9  
BI691631 775 bp mRNA linear EST 18-SEP-2001  
LOCUS 60330731.F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5343463 5',  
DEFINITION mRNA sequence.  
ACCESSION BI691631  
VERSION BI691631.1 GI:15654260  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC).  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: CGAPdb-rc@mail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM1872 row: K column: 04  
High quality sequence stop: 738.  
Location/Qualifiers

FEATURES  
source  
1..775  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_image="5343463"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/clone\_id="NCI\_CGAP\_Mam6"  
/notes="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN  
Query Match 79.2%; Score 19.8; DB 4; Length 775;  
Best Local Similarity 91.3%; Pred. No. 90;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTTCAACACCTGTAAATCC 23  
Db 604 AGCTTCAACACCTGTAAATCC 626

RESULT 10  
BH521842/c 526 bp DNA linear GSS 13-DEC-2001  
LOCUS BH521842  
DEFINITION BOGQF60F BOGQ Brassica oleracea genomic clone BOGQF60, genomic  
survey sequence.  
ACCESSION BH521842  
VERSION BH521842.1 GI:17729927  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Town, C.D., Van Aken, S., Uterback, T., Koc, H. and Fraser, C.M.  
TITLE Whole genome shotgun sequencing of Brassica oleracea  
JOURNAL Unpublished (2001)  
COMMENT Contact: Chris Town  
TRICR 9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@icr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TP  
Class: sheared ends.  
Location/Qualifiers

FEATURES  
source  
1..526  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone\_image="BOGQF60"  
/clone\_id="BOGQ"  
/notes="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared  
genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN  
Query Match 76.8%; Score 19.2; DB 8; Length 526;  
Best Local Similarity 87.5%; Pred. No. 176+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCAACACCTGTAAATCC 24  
Db 215 ATCTTATACACCTGTAAATCCT 192

RESULT 11  
AU291400 553 bp mRNA linear EST 04-DEC-2002  
LOCUS AU291400 zinnia cultured mesophyll cell equalized cDNA zinnia  
DEFINITION elegans cDNA clone Z6035, mRNA sequence.  
ACCESSION AU291400  
VERSION AU291400.1 GI:24251908  
KEYWORDS EST.  
SOURCE Zinnia elegans  
ORGANISM Zinnia elegans  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Zinnia.  
REFERENCE Demura, T., Tashiro, G., Horiguchi, G., Kishimoto, N., Kubo, M.,  
1 (bases 1 to 553) Matsuo, K., Minami, A., Nagata-Hiwatashi, M., Nakamura, K.,  
Okamura, Y., Sassa, N., Suzuki, S., Yazaki, J., Kikuchi, S. and  
Rukuda, H.  
TITLE Visualization by comprehensive microarray analysis of gene  
expression programs during transdifferentiation of mesophyll cells  
into xylem cells  
Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)  
CONTACT: Taku Demura  
Morphogenesis Research Group  
RIKEN Plant Science Center  
1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9605  
Fax: 81-45-503-9573  
Email: demura@postman.riken.go.jp  
This clone was obtained at our laboratory.  
Seq primer: M13 forward  
Location/Qualifiers

FEATURES  
source  
1..553  
/organism="Zinnia elegans"  
/mol\_type="mRNA"  
/cultivar="Canary bird"

ORIGIN

Query Match 76.8%; Score 19.2; DB 1; Length 553;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

/db\_xref="taxon:34245"  
 /clone="26035"  
 /issue\_type="mesophyll cell"  
 /clone\_lib="zinnia cultured mesophyll cell equalized cDNA"  
 /note="Vector: pGEM-T easy; cultured in tracheary element  
 differentiation-inductive medium"

QY 1 AGCTTCACACCGTGTAAATCCT 24  
 |||||  
 18 AGCTTCACACCGTGTAAATCCT 41

## RESULT 12

BH174634 589 bp DNA linear GSS 09-OCT-2001  
 LOCUS BH174634  
 DEFINITION B1751B20 Mouse IRS-PCR fragment library 57R/b1r Mus musculus  
 genomic clone B1751B20, genomic survey sequence.

ACCESSION BH174634  
 VERSION BH174634.1 GI:15990001  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 589)  
 Schalkwyk, L.C., Cusack, B., Dunkel, I., Hopp, M., Kramer, M.,  
 Palczewski, S., Pleffe, J., Scheel, S., Weiher, M., Wenske, G.,  
 Lehrach, H. and Himmelbauer, H.  
 Advanced integrated mouse YAC map including BAC framework  
 Genome Res. 11 (12), 2142-2150 (2001)

TITLE JOURNAL  
 MEDLINE 21588072  
 PUBMED 11731506

## COMMENT

Contact: Heinz Himmelbauer  
 Department of Vertebrate Genomics/ Abtig. Lehrach  
 Max-Planck-Institute of Molecular Genetics  
 Ihnestr.73, D-14195 Berlin-Dahlem, Germany  
 Email: himmelbauer@molgen.mpg.de  
 Information on marker localization (Chromosome, map segment) and on  
 YACs positive for this probe can be obtained from our web site  
 http://www.molgen.mpg.de/(tlide)rodent  
 Class: B1-PCR.

## FEATURES

## source

Location/Qualifiers  
 1..589  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="B1751B20"  
 /lab\_host="E.coli DH5alpha"  
 /clone\_id="Mouse IRS-PCR fragment library 57R/b1r"  
 /note="Vector: PAMPI0 (Gibco-BRL); The library was  
 generated from IRS-PCR fragments obtained by amplification  
 of genomic mouse DNA with the mouse B1-repeat primer B1R  
 (5'-AGTTCACACGACGCGGTATACGA-3'). Additional  
 information online at  
 www.molgen.mpg.de/~rodent/html/introduction.html"

## ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 589;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGTGTAAATCCT 24  
 |||||  
 Db 127 AGCTTCACACCGTGTAAATCCT 150

## RESULT 13

BH713924 604 bp DNA linear GSS 20-FEB-2002  
 LOCUS BH713924  
 DEFINITION BOMC138TR BO 2.3 KB Brassica oleracea genomic clone BOMC138,  
 genomic survey sequence.  
 ACCESSION BH713924  
 VERSION BH713924.1 GI:18806913  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 604)  
 Town, C.D., Van Aken, S., Uteirback, T., Koo, H. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other\_GSSs: BOMC138TR  
 Contact: Chris Town  
 TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TP  
 Class: sheared ends.

FEATURES  
 source Location/Qualifiers  
 1..604  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO100DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOMC138"  
 /clone\_id="BO 2.3 KB"  
 /note="Vector: pROS1, Site 1; Bext1; 2-3 kb sheared  
 genomic DNA inserted into pROS1 using Bext1 linkers"

## ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 604;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGTGTAAATCCT 24  
 |||||  
 Db 100 ATCTTATACACGCTGTAAATCCT 123

## RESULT 14

BH696214 617 bp DNA linear GSS 20-FEB-2002  
 LOCUS BH696214  
 DEFINITION BOMNB04TR BO 2.3 KB Brassica oleracea genomic clone BOMNB04,  
 genomic survey sequence.  
 ACCESSION BH696214  
 VERSION BH696214.1 GI:18768830  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 617)  
 Town, C.D., Van Aken, S., Uteirback, T., Koo, H. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other\_GSSs: BOMNB04TR  
 Contact: Chris Town  
 TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TP

Class: sheared ends.

FEATURES  
Location/Qualifiers

1..617  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOMNB04"  
/clone\_id="BO\_2\_3\_KB"  
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared  
genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 617;

Best Local Similarity 87.5%; Pred. No. 1.7e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGTGAATCCT 24  
181 ATCTATACACCGTGAATCCT 204

RESULT 15

BH698731 634 bp DNA linear GSS 20-FEB-2002

LOCUS BOMC167TF BO\_2\_3\_KB Brassica oleracea genomic clone BOMC167,

DEFINITION genomic survey sequence.

ACCESSION BH698731

VERSION BH698731.1 GI:18773206

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 634)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

COMMENT Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1..634  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOMC167"  
/clone\_id="BO\_2\_3\_KB"  
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared  
genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 634;

Best Local Similarity 87.5%; Pred. No. 1.7e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGTGAATCCT 24  
65 ATCTATACACCGTGAATCCT 88

Search completed: February 9, 2005, 21:55:40

Job time : 2451.85 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 1 gtcacatttcacgacacgacga 25

Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapex 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmb1.\*  
1: gb\_da.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_pl.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_str.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_y1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	AX504310	Sequence
2	25	100.0	25	AX504327	Sequence
3	25	100.0	765	AX706976	Sequence
4	25	100.0	765	AX707906	Sequence
5	25	100.0	765	HUMDBR1A11	Sequence
6	25	100.0	768	AY490254	Sequence
7	25	100.0	3489	AB029153	Sequence
8	25	100.0	3489	AB029153	Sequence
9	25	100.0	3489	AB029153	Sequence
10	25	100.0	3489	AB029153	Sequence
11	25	100.0	3489	AB029153	Sequence
12	25	100.0	3489	AB029153	Sequence
13	25	100.0	3489	AB029153	Sequence
14	25	100.0	3489	AB029153	Sequence
15	25	100.0	3489	AB029153	Sequence
16	25	100.0	3489	AB029153	Sequence
17	25	100.0	3489	AB029153	Sequence
18	25	100.0	3489	AB029153	Sequence
19	25	100.0	3489	AB029153	Sequence

c	20	25	100.0	4643	6	C0815440	Sequence
c	21	25	100.0	4643	6	AX522070	Sequence
c	22	25	100.0	4643	6	AX587788	Sequence
c	23	25	100.0	4646	6	BD234195	Sequence
c	24	25	100.0	4646	6	BD234195	Sequence
c	25	25	100.0	4646	6	BD234195	Sequence
c	26	25	100.0	4646	6	BD234195	Sequence
c	27	25	100.0	4646	6	BD234195	Sequence
c	28	25	100.0	4646	6	BD234195	Sequence
c	29	25	100.0	4646	6	BD234195	Sequence
c	30	25	100.0	4646	6	BD234195	Sequence
c	31	25	100.0	4646	6	BD234195	Sequence
c	32	25	100.0	4646	6	BD234195	Sequence
c	33	25	100.0	4646	6	BD234195	Sequence
c	34	25	100.0	4646	6	BD234195	Sequence
c	35	25	100.0	4646	6	BD234195	Sequence
c	36	25	100.0	4646	6	BD234195	Sequence
c	37	25	100.0	4646	6	BD234195	Sequence
c	38	25	100.0	4646	6	BD234195	Sequence
c	39	25	100.0	4646	6	BD234195	Sequence
c	40	25	100.0	4646	6	BD234195	Sequence
c	41	25	100.0	4646	6	BD234195	Sequence
c	42	25	100.0	4646	6	BD234195	Sequence
c	43	25	100.0	4646	6	BD234195	Sequence
c	44	25	100.0	4646	6	BD234195	Sequence
c	45	25	100.0	4646	6	BD234195	Sequence

#### ALIGNMENTS

RESULT 1	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
DEFINITION	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
ACCESSION	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
VERSION	AX504310.1	GI:23386128	25 bp	DNA	linear	PAT 27-SEP-2002
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
DB						
RESULT 2	AX504327/c	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504327	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
DEFINITION	AX504327	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
ACCESSION	AX504327	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
VERSION	AX504327.1	GI:23386139	25 bp	DNA	linear	PAT 27-SEP-2002
KEYWORDS						
SOURCE						
ORGANISM						

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	Colgan,S.P.
JOURNAL	Compositions and methods for treating hematologic malignancies and multiple drug resistance
FEATURES	Patent: WO 0234291-A 30 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
source	Location/Qualifiers 1..25 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN	
Query Match	100.0%; Score 25; DB 6; Length 25;
Best Local Similarity	100.0%; Pred.No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GTGACATTTTCACGGCCCATAGCGAA 25       25 GTGACATTTTCACGGCCCATAGCGAA 1
Dd	
RESULT 3	
AX706976/c	765 bp DNA linear PAT 04-APR-2003
LOCUS	Sequence 674 from Patent WO03013534.
DEFINITION	AX706976
ACCESSION	AX706976.1 GI:29563301
VERSION	
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	Heinrich,G. and Kerb,R.
JOURNAL	Methods for the treatment of cancer with irinotecan based on CYP3A5
FEATURES	Patent: WO 03013534-A 674 20-FEB-2003; Epidaurus Biotechnology AG (DE) Location/Qualifiers 1..765 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN	
Query Match	100.0%; Score 25; DB 6; Length 765;
Best Local Similarity	100.0%; Pred.No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GTGACATTTTCACGGCCCATAGCGAA 25       672 GTGACATTTTCACGGCCCATAGCGAA 648
Dd	
RESULT 4	
AX707906/c	765 bp DNA linear PAT 04-APR-2003
LOCUS	Sequence 674 from Patent WO03013536.
DEFINITION	AX707906
ACCESSION	AX707906.1 GI:29563981
VERSION	
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	Heinrich,G. and Kerb,R.
JOURNAL	Methods for treatment of cancer using irinotecan based on UGT1A1
FEATURES	Patent: WO 03013536-A 674 20-FEB-2003; Epidaurus Biotechnology AG (DE) Location/Qualifiers

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Oy	1 GTGACATTTTCAGCGCCATTAGCGAA 25	
Db	672 GTGACATTTTCAGCGCCATTAGCGAA 648	
RESULT 5	HMMMDR1A1/c	
LOCUS	HUMMDR1A11	765 bp     DNA     linear     PRI 08-JAN-1995
DEFINITION	Human P-glycoprotein (MDR1) gene, exon 11, 12 and 13.	
ACCESSION	M29432 J05168	
VERSION	M29432.1 GI:187481	
KEYWORDS	P-glycoprotein; multidrug resistance.	
SEGMENT	11 OF 26	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
1 (bases 280 to 437)		
Chin,J.E., Seffir,R., Noonan,K.E., Choi,K. and Roninson,I.B.		
Structure and expression of the human MDR (P-glycoprotein) gene		
family		
Mol. Cell. Biol. 9 (9), 3808-3820 (1989)		
JOURNAL	89384608	
MEDLINE	2571078	
PUBMED	2 (bases 1 to 765)	
REFERENCE	Chen,C.J., Clark,D., Ueda,K., Pastan,I., Gottesman,M.M. and	
AUTHORS	Roninson,I.B.	
TITLE	Genomic organization of the human multidrug resistance (MDR1) gene	
JOURNAL	and origin of P-glycoproteins	
MEDLINE	J. Biol. Chem. 265 (1), 506-514 (1990)	
PUBMED	90094448	
COMMENT	1967175	
DNA.	Original source text: Human multidrug resistant cell line KB-VI	
Draft entry and computer-readable sequence for [1] kindly submitted		
by I.B.Roninson, 27-OCT-1989.		
location/Qualifiers		
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	/note="PGY1, intron L"	
exon	536..739	



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/note="PGY1, Interon M"

ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 765;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
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Qy 1 GTGACATTTTCACGGCCATAGCGAA 25  
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Db 672 GTGACATTTTCACGGCCATAGCGAA 648

RESULT 6  
AY490254/c 768 bp DNA linear PRI 27-JAN-2004  
LOCUS Homo. sapiens P-glycoprotein (MDR1) gene, partial cds.  
DEFINITION  
ACCESSION AY490254  
VERSION AY490254.1 GI:41058414  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Homo sapiens  
TITLE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 768)  
Direct Submission  
Submitted (30-NOV-2003) Human Molecular Genetics, Rajiv Gandhi  
Centre for Biotechnology, Thycaud P.O., Thiruvananthapuram, Kerala  
695014, India  
Location/Qualifiers  
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/note="transporter"  
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ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 768;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25  
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Db 675 GTGACATTTTCACGGCCATAGCGAA 651

RESULT 7  
AB029153/c 3489 bp mRNA linear MAM 28-MAR-2002  
LOCUS Felis catus multi-drug resistance related mRNA, partial cds.  
DEFINITION  
ACCESSION AB029153

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
2 (bases 1 to 3489)  
Tsujimoto, H. and Okai, Y.  
Direct Submission  
Submitted (05-JUN-1999) Hajime Tsujimoto, The University of Tokyo,  
Department of Veterinary Internal Medicine; The University of  
Tokyo, Bunkyo-ku, Tokyo 113-8657, Japan  
(E-mail:atsuji@hongo.ecc.u-tokyo.ac.jp, Tel: +81-3-5841-8004,  
Fax: +81-3-5841-8178)  
Location/Qualifiers  
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MAGVILIDGKEIKHLNVQMLRAHMGIVSOPFIFDCSIGENIAYGDSRVVSGEYIR  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1310 GTGACATTTTCACGGCCATAGCGAA 1286

RESULT 8  
AX481416/c 3840 bp DNA linear PAT 16-AUG-2002  
LOCUS Sequence 30 from Patent WO02055693.  
DEFINITION  
ACCESSION AX481416  
VERSION AX481416.1 GI:22316330  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Haefliger, P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 0205693-A 30 18-JUL-2002;  
Ribopharma AG (DE)

FEATURES  
source  
1. 3840  
/organism="Homo sapiens"  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1484 GTGACATTTTCACGGCCATAGCGAA 1460

RESULT 9  
BD171402/c  
LOCUS BD171402 3843 bp DNA linear PAT 18-FEB-2003  
DEFINITION Method for predicting side effects of immunosuppressant and primer  
used therefor.  
ACCESSION BD171402  
VERSION BD171402.1 GI:28412692  
KEYWORDS JP 2002223769-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Teiri, I.  
TITLE Method for predicting side effects of immunosuppressant and primer  
used therefor  
JOURNAL Patent: JP 2002223769-A 1 13-AUG-2002;  
SRL INC

COMMENT OS Homo sapiens (human)  
PN JP 2002223769-A/1  
PD 13-AUG-2002  
PF 31-JAN-2001 JP 2001024723  
PI ICHIRO TEIRI  
PC C12N15/09,C1201/68,C12N15/00  
CC Method for predicting side effects of immunosuppressant and  
CC primer used  
CC therefor  
FH Key  
FT source  
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/mol\_type="genomic DNA"  
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1. 3843  
Location/Qualifiers  
1. 3843  
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Best Local Similarity 100.0%; Pred. No. 0.2;  
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QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 10  
AX322787/c  
LOCUS AX322787 3860 bp DNA linear PAT 07-JAN-2002

DEFINITION Sequence 1 from Patent WO0192877.  
ACCESSION AX322787  
VERSION AX322787.1 GI:18093766  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Sorrentino, B. and Schuetz, J.  
TITLE Method of identifying and/or isolating stem cells  
JOURNAL Patent: WO 0192877-A 1 06-DEC-2001;  
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)

FEATURES  
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1. 3860  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 11  
AX322789/c  
LOCUS AX322789 3860 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 3 from Patent WO0192877.  
ACCESSION AX322789  
VERSION AX322789.1 GI:18093767  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Sorrentino, B. and Schuetz, J.  
TITLE Method of identifying and/or isolating stem cells  
JOURNAL Patent: WO 0192877-A 3 06-DEC-2001;  
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)

FEATURES  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 12  
BD190394/c  
LOCUS BD190394 3988 bp DNA linear PAT 17-JUL-2003  
DEFINITION Phosphatidylcholine as a medicament for the protection of mucosa.  
ACCESSION BD190394  
VERSION BD190394.1 GI:33000133  
KEYWORDS JP 2002522381-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
(bases 1 to 3988)

**AUTHORS** Stremmel, W.  
**TITLE** Phosphatidylcholine as a medicament for the protection of mucosa  
**JOURNAL** Patent: JP 2002522381-A 1 23-JUL-2002;  
 Wolfgang STREMMEL  
**COMMENT** OS Homo Sapiens  
 PN JP 2002522381-A/1  
 PD 23-JUL-2002  
 PF 06-AUG-1999 JP 2000563262  
 PR 06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DE 198 57 750.8 PI  
 Wolfgang stremmel  
**CC**

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 Db 1553 GTGACATTTTCACGGCCATAGCGAA 1529

**RESULT 13**  
 AR452556/c 3988 bp DNA linear PAT 20-FEB-2004  
**LOCUS** AR452556  
**DEFINITION** Sequence 1 from patent US 6677319.  
**ACCESSION** AR452556  
**VERSION** AR452556.1 GI:42684344  
**KEYWORDS**  
**SOURCE** Unknown.  
**ORGANISM** Unknown.  
**REFERENCE** 1 (bases 1 to 3988)  
**AUTHORS** Stremmel, W.  
**TITLE** Phosphatidylcholine as medication with protective effect large  
**JOURNAL** Patent: US 6677319-A 1 13-JAN-2004;  
**FEATURES** Location/Qualifiers  
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**ORIGIN**

Query Match 100.0%; Score 25; DB 6; Length 3988;  
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**RESULT 14**  
 AX024454/c 3988 bp DNA linear PAT 15-SEP-2000  
**LOCUS** AX024454  
**DEFINITION** Sequence 1 from Patent DE19857750.  
**ACCESSION** AX024454  
**VERSION** AX024454.1 GI:10184622  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1  
**AUTHORS** Stremmel, W.  
**JOURNAL** Patent: DE 19857750-A 1 24-FEB-2000;  
 STREMMEL WOLFGANG (DE)

**FEATURES** Location/Qualifiers  
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 Db 1553 GTGACATTTTCACGGCCATAGCGAA 1529

**RESULT 15**  
 AF016535/c 4192 bp mRNA linear PRI 03-SEP-1997  
**LOCUS** AF016535  
**DEFINITION** Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds.  
**ACCESSION** AF016535  
**VERSION** AF016535.1 GI:2353263  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 4192)  
**AUTHORS** Chen, C.J., Chin, J.E., Ueda, K., Clark, D.P., Pastan, I.,  
 Gottesman, M.M. and Roninson, I.B.  
**TITLE** Internal duplication and homology with bacterial transport proteins  
 in the mdr1 (P-glycoprotein) gene from multidrug-resistant human  
 cells  
**JOURNAL** Cell 47 (3), 381-389 (1986)  
**MEDLINE** 87028230  
**PUBMED** 2876781  
**REFERENCE** 2 (bases 1 to 4192)  
**AUTHORS** Chen, G., Duran, G.E., Steger, K.A., Lacayo, N.J., Jaffrezou, J.P.,  
 Dumontet, C. and Sikic, B.I.  
**TITLE** Multidrug-resistant human sarcoma cells with a mutant  
 P-glycoprotein, altered phenotype, and resistance to cyclosporins  
**JOURNAL** J. Biol. Chem. 272 (9), 5974-5982 (1997)  
**MEDLINE** 97190336  
**PUBMED** 9038218  
**REFERENCE** 3 (bases 1 to 4192)  
**AUTHORS** Chen, G., Lacayo, N.J., Steger, K.A. and Sikic, B.I.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (28-JUL-1997) Medicine, Stanford University School of  
 Medicine, Stanford, CA 94306, USA  
**FEATURES** Location/Qualifiers  
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FEHMYAQSLOVPYNSLRKAHIFGITFSFOAMMYFSYACGFRGAYLVAKHLMSEFED  
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659

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTACGGCCATAGCGAA 25  
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Db 1603 GTGACATTTACGGCCATAGCGAA 1579

Search completed: February 9, 2005, 17:02:01  
Job time : 482.178 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 78.592 Seconds  
(without alignments)  
520.498 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 25  
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Scoring table: IDENTITY NUC  
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Searched: 1202784 seqs, 81813359 residues

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Listing first 45 summaries

Database: Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	3988	4 US-09-762-195-1	Sequence 1, Appli
C 2	25	100.0	4284	2 US-08-784-649A-1	Sequence 1, Appli
C 3	25	100.0	4264	2 US-08-784-649A-5	Sequence 5, Appli
C 4	25	100.0	4646	1 US-08-181-471-2	Sequence 2, Appli
C 5	25	100.0	4664	4 US-09-023-655-1167	Sequence 1167, Ap
C 6	25	100.0	4669	2 US-08-583-276-18	Sequence 18, Appli
C 7	25	100.0	4669	2 US-08-752-447-1	Sequence 1, Appli
C 8	25	100.0	4669	3 US-09-316-167-1	Sequence 1, Appli
C 9	25	100.0	4669	4 US-09-397-233-1	Sequence 1, Appli
C 10	25	100.0	4669	6 5206352-3	Patent No. 5206352
C 11	25	100.0	4669	2 US-08-793-610-5	Sequence 5, Appli
C 12	25	100.0	8630	4 US-09-306-417-2	Sequence 2, Appli
C 13	25	100.0	8630	4 US-09-306-417-2	Sequence 2, Appli
C 14	25	100.0	8630	4 US-09-306-417-2	Sequence 2, Appli
C 15	25	100.0	9318	2 US-08-793-610-6	Sequence 6, Appli
C 16	25	100.0	9318	4 US-09-672-725C-1	Sequence 1, Appli
C 17	25	100.0	9318	4 US-09-672-725C-1	Sequence 1, Appli
C 18	25	100.0	9318	4 US-09-672-725C-22	Sequence 22, Appli
C 19	25	100.0	9318	4 US-09-672-725C-26	Sequence 26, Appli
C 20	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 21	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 22	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 23	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 24	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 25	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 26	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli
C 27	25	100.0	9318	4 US-09-672-725C-3	Sequence 3, Appli

C 28	21.8	87.2	4233	3 US-09-120-513-1	Sequence 1, Appli
C 29	21.8	87.2	4233	3 US-09-450-105-1	Sequence 1, Appli
C 30	19	76.0	3321	4 US-09-640-173-175	Sequence 175, App
C 31	19	76.0	3321	4 US-09-713-550-175	Sequence 175, App
C 32	19	76.0	3321	4 US-09-825-294-175	Sequence 175, App
C 33	19	76.0	3321	4 US-09-970-966-175	Sequence 175, App
C 34	18.6	74.4	3924	4 US-09-023-655-1168	Sequence 1168, Ap
C 35	18.6	74.4	3924	4 US-09-762-195-2	Sequence 2, Appli
C 36	18.2	72.8	601	4 US-09-949-016-61079	Sequence 61079, A
C 37	18.2	72.8	723	4 US-09-016-434-1422	Sequence 1422, Ap
C 38	18.2	72.8	1255	4 US-09-949-016-1772	Sequence 1772, Ap
C 39	18.2	72.8	1446	3 US-08-787-091-1	Sequence 1, Appli
C 40	18.2	72.8	8137	4 US-09-566-921-7	Sequence 7, Appli
C 41	18.2	72.8	47698	4 US-09-949-016-13514	Sequence 13514, A
C 42	17.8	71.2	26	1 US-08-227-370-4	Sequence 4, Appli
C 43	17.8	71.2	26	5 PCT-US94-06284-4	Sequence 4, Appli
C 44	17.6	70.4	945	4 US-09-134-000C-186	Sequence 186, App
C 45	17.4	69.6	616	4 US-09-270-767-11434	Sequence 11434, A

## ALIGNMENTS

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RESULT 1
US-09-762-195-1/c
; Sequence 1, Application US/09762195
; Patent No. 6677319
; GENERAL INFORMATION:
; APPLICANT: Streemmel, Wolfgang
; TITLE OF INVENTION: Phosphatidylcholine as Medication with
; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US/09/762,195
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: PCT/EP9702426
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-1
Query Match 100.0%; Score 25; DB 4; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative
QY 1 GTGACATTTTCACGCCCATAGCGAA 25
Db 1553 GTGACATTTTCACGCCCATAGCGAA 1529
RESULT 2
US-08-784-649A-1/c
; Sequence 1, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Sikic, Branimir I
; TITLE OF INVENTION: P-Glycoprotein Mutant Resistant to
; TITLE OF INVENTION: Cyclosporin Modulation
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
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ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,649A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: Reg.No. 5830697 36,677  
REFERENCE/DOCKET NUMBER: 06037/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4264 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-784-649A-1

Query Match 100.0%; Score 25; DB 2; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1625 GTGACATTTTCACGGCCATAGCGAA 1601

RESULT 3  
US-08-784-649A-5/c  
Sequence 5, Application US/08784649A  
Patent No. 5830697  
GENERAL INFORMATION:  
APPLICANT: Sixic, Branlmitr I  
APPLICANT: Chen, Gang  
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO  
TITLE OF INVENTION: CYCLOSPORIN MODULATION  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,649A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: Reg.No. 5830697 36,677  
REFERENCE/DOCKET NUMBER: 06037/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4264 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1625 GTGACATTTTCACGGCCATAGCGAA 1601

RESULT 4  
US-08-181-471-2/c  
Sequence 2, Application US/08181471  
Patent No. 5641508  
GENERAL INFORMATION:  
APPLICANT: Li, Lingna  
APPLICANT: Liebko, Valeryi K.  
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL  
TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Thomas Fitting  
STREET: 12526 High Bluff Drive, Suite 300  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92130  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,471  
FILING DATE: 13-JAN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/041,553  
FILING DATE: 02-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: ANT0023P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-792-3680  
TELEFAX: 619-792-8477  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4646 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4267  
US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 5

US-09-023-655-1167/c  
 / Sequence 1167, Application US/09023655  
 / Patent No. 6607879  
 / GENERAL INFORMATION:  
 / APPLICANT: Cocke, Benjamin G.  
 / APPLICANT: Susan G. Stuart  
 / APPLICANT: Jeffrey J. Seihamer  
 / TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 / NUMBER OF SEQUENCES: 1508  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 / STREET: 3174 PORTER DRIVE  
 / CITY: PALO ALTO  
 / STATE: CALIFORNIA  
 / COUNTRY: USA  
 / ZIP: 94304  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/023,655  
 / FILING DATE: HEREMITH  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER:  
 / FILING DATE:  
 / CLASSIFICATION:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Zeller, Karen J.  
 / REGISTRATION NUMBER: 37,071  
 / REFERENCE/DOCKET NUMBER: PA-0001 US  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (650) 855-0555  
 / TELEFAX: (650) 845-4166  
 / INFORMATION FOR SEQ ID NO: 1167:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4646 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / IMMEDIATE SOURCE:  
 / LIBRARY: GENBANK  
 / CLONE: 9187468  
 / US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCAGCGCCATAGCGAA 25  
 DB 1911 GTGACATTTTCAGCGCCATAGCGAA 1887

RESULT 6  
 US-08-583-276-18/c  
 / Sequence 18, Application US/08583276  
 / Patent No. 5837536  
 / GENERAL INFORMATION:  
 / APPLICANT: McDonagh, Kevin T.  
 / APPLICANT: Nienhuis, Arthur  
 / APPLICANT: Tolstoshev, Paul  
 / TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
 / TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
 / TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES  
 / NUMBER OF SEQUENCES: 19  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
 / ADDRESSEE: Cecchi & Stewart  
 / STREET: 6 Becker Farm Road

CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07068  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: 3.5 inch diskette  
 / OPERATING SYSTEM: PC-DOS  
 / SOFTWARE: DM4 V2  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/583,276  
 / FILING DATE: 05-JAN-1996  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/332,444  
 / FILING DATE: 31-OCT-1994  
 / APPLICATION NUMBER: 07/887,712  
 / FILING DATE: 22-MAY-1992  
 / INFORMATION FOR SEQ ID NO: 18:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4669 bases  
 / TYPE: nucleic acid  
 / STRANDEDNESS: singular  
 / TOPOLOGY: linear  
 / MOLECULE TYPE:  
 / DESCRIPTION: Genomic DNA  
 / US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCAGCGCCATAGCGAA 25  
 DB 1911 GTGACATTTTCAGCGCCATAGCGAA 1887

RESULT 7  
 US-08-752-447-1/c  
 / Sequence 1, Application US/08752447  
 / Patent No. 5994088  
 / GENERAL INFORMATION:  
 / APPLICANT: Mecheiner, Eugene  
 / APPLICANT: Robinson, Igor B  
 / TITLE OF INVENTION: Methods and Reagents for Preparing and  
 / TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
 / NUMBER OF SEQUENCES: 2  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
 / STREET: 300 South Wacker Drive, Seventh Floor  
 / CITY: Chicago  
 / STATE: Illinois  
 / COUNTRY: USA  
 / ZIP: 60606  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / OPERATING SYSTEM: IBM PC compatible  
 / SOFTWARE: Patentin Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/752,447  
 / FILING DATE: 15-NOV-1996  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: No. 5994088nan, Kevin E  
 / REGISTRATION NUMBER: 35,303  
 / REFERENCE/DOCKET NUMBER: 95,1121  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 312-913-9608  
 / TELEFAX: 312-913-0001  
 / INFORMATION FOR SEQ ID NO: 1:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4669 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGCCCATAGCGAA 25  
DB 1911 GTGACATTTTCACGCCCATAGCGAA 1887

RESULT 8  
US-09-316-167-1/c  
Sequence 1, Application US/09316167  
Patent No. 6365357  
GENERAL INFORMATION:  
APPLICANT: Mechettner, Eugene  
APPLICANT: Roninson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/316.167  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752.447  
FILING DATE: 15-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6365357nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-9808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264

FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGCCCATAGCGAA 25  
DB 1911 GTGACATTTTCACGCCCATAGCGAA 1887

RESULT 9  
US-09-397-233-1/c  
Sequence 1, Application US/09397233  
Patent No. 6630327  
GENERAL INFORMATION:  
APPLICANT: Mechettner, Eugene  
APPLICANT: Roninson, Igor B  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/397.233  
FILING DATE: 16-Sep-1999  
CLASSIFICATION: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6630327nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-397-233-1  
Query Match 100.0%; Score 25; DB 4; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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RESULT 10
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO:3:
LENGTH: 4669
5206352-3

Query Match          100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 11
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO:3:
LENGTH: 4669
5206352-3

Query Match          100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 12
US-08-793-610-5/c
Sequence 5, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERING, Wolfgang
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP

```

```

STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-5

Query Match          100.0%; Score 25; DB 2; Length 6505;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 3303 GTGACATTTTCACGGCCATAGCGAA 3279

RESULT 13
US-09-306-417-1/c
Sequence 1, Application US/09306417
Patent No. 6548301
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
OTHER INFORMATION: plasmid DNA
NAME/KEY: misc. feature
LOCATION: (1)-(160)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:

```

```
NAME/KEY: misc.feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (1220)..(5062)
OTHER INFORMATION: m4 mdr-1 CDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SFpeta71m4
US-09-306-417-1
```

```
Query Match 100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGACATTTTCACGGCCATTAGCGAA 25
DB 2706 GTGACATTTTCACGGCCATTAGCGAA 2682
```

```
RESULT 14
US-09-306-417-2/c
Sequence 2, Application US/09306417
Patent No. 6548301
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306.417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
OTHER INFORMATION: plasmid DNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SFpeta71m4
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (1220)..(5062)
OTHER INFORMATION: m4 mdr1 CDNA
```

```
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
US-09-306-417-2
```

```
Query Match 100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGACATTTTCACGGCCATTAGCGAA 25
DB 2706 GTGACATTTTCACGGCCATTAGCGAA 2682
```

```
RESULT 15
US-08-793-610-6/c
Sequence 6, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARRIS, Carol
APPLICANT: OSTERING, Wolfgang
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-6
```

```
Query Match 100.0%; Score 25; DB 2; Length 9318;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 GTGACATTTTCACGGCCATAGCGAA 25  
Db 3262 GTGACATTTTCACGGCCATAGCGAA 3238

Search completed: February 9, 2005, 17:11:18  
Job time : 79.592 secs

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PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
PT binding molecules.  
PS Claim 14; Page 43; 92pp; English.  
XX  
XX The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is an antisense  
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its  
CC expression. This oligo is used in the exemplification of the invention  
CC  
SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1 GTGACATTTTCACGGCCATAGCGAA 25  
RESULT 2  
AAD39012/c  
ID AAD39012 standard; DNA; 25 BP.  
XX  
AC AAD39012;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human mdrl gene HIF-1 binding site DNA #5.  
XX  
XX Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;  
XX hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;  
XX lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
XX myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;  
XX angiotenic myeloid metaplasia; myeloid leukaemia; gene therapy;  
XX polycythaemia vera; hypoxia responsive element; HRE; ds.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT misc\_binding 11..15  
FT /\*tag= a  
FT /bound\_moiety= "HIF-1"  
XX  
XX WO200234291-A2.  
XX  
XX 02-MAY-2002.  
XX  
XX 25-OCT-2001; 2001MO-US049856.  
XX  
XX 26-OCT-2000; 2000US-0243542P.  
XX  
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX  
XX Colgan SP;  
XX  
XX WPI; 2002-471427/50.  
XX  
XX Treating a subject (at risk of) having a hematologic malignancy or  
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
PT binding molecules.  
PS Example 2; Page 12; 92pp; English.  
XX  
XX The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is human mdrl  
CC gene HIF-1 binding site DNA  
CC  
SQ Sequence 25 BP; 6 A; 6 C; 6 G; 7 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 25 GTGACATTTTCACGGCCATAGCGAA 1  
RESULT 3  
ACH82796  
ID ACH82796 standard; DNA; 219 BP.  
XX  
AC ACH82796;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human genome derived single exon probe #15991.  
XX  
XX Human; probe; ss; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.  
XX  
XX Homo sapiens.  
OS  
XX US2003194704-A1.  
XX  
XX 16-OCT-2003.  
XX  
XX 03-APR-2002; 2002US-00029386.  
XX  
XX 03-APR-2002; 2002US-00029386.  
XX  
XX (PENN/) PENN S G.  
XX (RANK/) RANK D R.  
XX (HANZ/) HANZEL D K.  
XX  
XX Penn SG, Rank DR, Hanzel DK;  
XX  
XX WPI; 2004-119264/12.  
XX  
XX New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.  
XX  
XX Claim 1; SEQ ID NO 15991; 80pp; English.  
XX  
XX The invention relates to a nucleic acid probe for measuring human gene  
CC expression, comprising any of the 27,400 fully defined nucleotide  
CC sequences in the specification, or their complements or fragments, and

CC	encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC	fully defined in the specification. The probe is a single exon probe that
CC	hybridises under high stringency conditions to a nucleic acid molecule
CC	expressed in human cells or tissues. Also included are a spatially-
CC	addressable set of single exon nucleic acid probes for measuring human
CC	cne expression (comprising a plurality of single exon nucleic acid
CC	probes cited above, where each of the plurality of probes is separately
CC	and addressably isolatable or amplifiable from the plurality), a single
CC	exon microarray for measuring human gene expression, a method of
CC	measuring human gene expression, a vector comprising the single exon
CC	probe cited above, an ORF-encoded peptide comprising at least 8
CC	continuous amino acids of any of the above-mentioned amino acid
CC	sequences (optionally with conservative amino acid substitutions), an
CC	isolated antibody that binds specifically to a peptide cited above,
CC	methods of seiling and/or licensing single exon probes or microarrays to
CC	a customer desiring to measure gene expression, a method of providing
CC	human gene expression data by subscription, and a computer-readable
CC	storage medium which contains a database having a plurality of records
CC	(each record including data on the expression of a single exon probe
CC	cited above. The probe, methods and apparatus are useful in gene
CC	expression analysis. The probes may be used as tools for surveying
CC	tissues to detect the presence of expressed messages that contain their
CC	specific exon, or in constructing genome-derived single exon microarrays.
CC	In addition, the probes are used in identifying and characterising
CC	alternative splicing events, in detecting and characterising gross
CC	alterations in the genomic locus that includes their exon, in assessing
CC	smaller genomic alterations, in pinning the synthesis of nucleic acids,
CC	or in expressing the ORF-encoded peptide. The present sequence is a human
CC	single exon probe of the invention. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from USPRO at
CC	Seqdata.uspto.gov/sequence.html?DocID=20030194704
SO	Sequence 219 BP; 61 A; 56 C; 38 G; 64 T; 0 U; 0 Other;
XX	
XX	
Query Match	100.0%; Score 25; DB 12; Length 219;
Best Local Similarity	100.0%; Pred. No. 0.02; Indels 0; Gaps 0
Matches 25; Conservative 0; Mismatches	
Oy	1 GTGACATTTTCAGCGCCATAGCGGA 25       77 GTGACATTTTCAGCGCCATAGCGGA 101
Dd	
RESULT 4	
ACH69096	ACH69096 standard; DNA; 584 BP.
XX	
XX	ACH69096;
XX	
DT	29-JUL-2004 (first entry)
XX	
DE	Human genome derived single exon probe #2291.
XX	
XX	Human; probe; ss; gene expression; single exon probe; microarray;
KW	alternative splicing event; genomic alteration.
OS	Homo sapiens.
PN	US2003194704-A1.
PD	16-OCT-2003.
PF	03-APR-2002; 2002US-00029386.
PR	03-APR-2002; 2002US-00029386.
PA	(PENN/) PENN S G.
PA	(RANK/) RANK D R.
PA	(HANZ/) HANZEL D K.
PI	Penn SG, Rank DR, Hanzel DK;
XX	

XX WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

PS Claim 15; SEQ ID NO 2291; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

XX expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 688 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), an

CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable

CC storage medium which contains a database having a plurality of records

CC (each record including data on the expression of a single exon probe

CC cited above). The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.

CC In addition, the probes are used in identifying and characterising

CC alternative splicing events, in detecting and characterising gross

CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,

CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from USPTO at

CC segdata.uspto.gov/sequence.html?docID=20030194704

XX  
XX  
SQ Sequence 584 BP; 166 A; 139 C; 100 G; 179 T; 0 U; 0 Other;

OY 1 GTGACATTTTCAGCGCATAGCGAA 25  
|||||  
DB 320 GTGACATTTCACGGCACAAGCGAA 344

Query Match 100.0%; Score 25; DB 12; Length 584;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 5  
AAA96071/c  
ID AAA96071 standard; DNA; 765 BP.  
XX AAA96071;  
DT 29-JAN-2001 (first entry)  
XX Human Pgp ATP binding cassette (ABC) transporter coding sequence.  
KW Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;  
KM human; ATP binding cassette; ABC transporter; de.  
OS Homo sapiens.  
XX  
XX WO200052144-A1.  
XX

PD 08-SEP-2000.  
 XX  
 PF 26-FEB-2000; 2000WO-US005315.  
 XX  
 PR 03-MAR-1999; 99US-00261825.  
 XX  
 PA (TEXA ) UNIV TEXAS.  
 XX  
 PI Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;  
 XX  
 DR WPI; 2000-587306/55.  
 XX  
 PT Increasing or decreasing drug resistance in target bacteria, yeast, plant  
 PT or mammalian cells comprises altering ATP gradient across biological  
 PT membrane of target cell.  
 XX  
 PS Claim 15, Page; 85pp; English.  
 XX  
 CC The present invention relates to a method for increasing or decreasing  
 CC drug resistance in target bacteria, yeast, plant or mammalian cells by  
 CC altering the ATP gradient across the biological membrane of the target  
 CC cell. The method is useful for modulating drug resistance of cells. It is  
 CC useful for increasing the sensitivity of cells to chemotherapeutic and  
 CC antibiotic agents and increasing resistance to herbicides. The present  
 CC sequence is human Rgp ATP binding cassette (ABC) transporter coding  
 CC sequence. This sequence was used in the present invention to modulate  
 CC drug resistance. Note: The present sequence is not shown in the  
 CC specification, but is referred to via its Genbank accession number  
 CC  
 XX  
 SQ Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 3; Length 765;  
 Best Local Similarity 100.0%; Pred. No. 0.026;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
 DB 672 GTGACATTTTCACGGCCATAGCGAA 648  
 RESULT 6  
 ACF62746/c  
 ID ACF62746 standard; DNA; 765 BP.  
 XX  
 AC ACF62746;  
 XX  
 DT 08-OCT-2003 (first entry)  
 XX  
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:674.  
 XX  
 KM Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;  
 KM cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;  
 KM cytoskeletal; gene; ds.  
 XX  
 OS Undentified.  
 XX  
 PN WO2003013534-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 23-JUL-2002; 2002WO-EP008219.  
 XX  
 PR 23-JUL-2001; 2001EP-00117608.  
 PR 24-MAY-2002; 2002EP-00011710.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Heinrich G, Kerb R;  
 XX  
 DR WPI; 2003-268144/26.  
 XX  
 PT New use of irinotecan for preparation of compositions for treating cancer  
 PT in subject having genome with variant allele comprising cytochrome p450,

PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.  
 XX  
 XX Disclosure; SEQ ID NO 674; 86pp; English.  
 XX  
 CC The present invention describes the use of irinotecan (I) or its  
 CC derivative for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject having a genome with a variant  
 CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine  
 CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have  
 CC cytostatic activity. The therapeutic applications of (I) is improved,  
 CC since it is possible to individually treat a subject with an appropriate  
 CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,  
 CC harmful or toxic effects are efficiently avoided. Unnecessary and  
 CC potentially harmful treatment of those subjects who do not respond to the  
 CC treatment with substances (nonresponders), as well as the development of  
 CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200  
 CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the  
 CC exemplification of the present invention  
 CC  
 XX  
 SQ Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 8; Length 765;  
 Best Local Similarity 100.0%; Pred. No. 0.026;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
 DB 672 GTGACATTTTCACGGCCATAGCGAA 648  
 RESULT 7  
 ADB20861/c  
 ID ADB20861 standard; DNA; 765 BP.  
 XX  
 AC ADB20861;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE MRP1 based cancer related nucleic acid SEQ ID NO:674.  
 XX  
 KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
 KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
 KM variant allele; multidrug resistance protein 1; MRP1; cytoskeletal; gene;  
 KM ds.  
 XX  
 OS Undentified.  
 XX  
 PN WO2003013533-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 23-JUL-2002; 2002WO-EP008200.  
 XX  
 PR 23-JUL-2001; 2001EP-00117608.  
 PR 24-MAY-2002; 2002EP-00011710.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Heinrich G, Kerb R;  
 XX  
 DR WPI; 2003-354397/33.  
 XX  
 PT Use of irinotecan or its derivative for preparation of a pharmaceutical  
 PT composition for treating cancer in a subject having a genome with a  
 PT variant allele comprising a multidrug resistance protein 1  
 PT polynucleotide.  
 XX  
 PS Disclosure; SEQ ID NO 674; 100pp; English.  
 XX  
 CC The present invention describes a method for the use of irinotecan (I) or  
 CC its derivative for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic



CC cancer, or malignant glioma in a subject having a genome with a variant  
 CC allele which comprises a multidrug resistance protein 1 (MRP1)  
 CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative  
 CC can be used for the preparation of a pharmaceutical composition for  
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
 CC cancer, or malignant glioma in a subject, where the subject is a human  
 CC (preferably African or Asian) or a mouse. The present sequence represents  
 CC a sequence which is used in the exemplification of the present invention.  
 CC  
 XX  
 XX Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;  
 Qy Query Match 100.0%; Score 25; DB 8; Length 765;  
 Best Local Similarity 100.0%; Pred. No. 0.026;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 Db 672 GTGACATTTTCAGCGCCATAGCGAA 25  
 672 GTGACATTTTCAGCGCCATAGCGAA 648  
 RESULT 8  
 ADB87950/C  
 ID ADB87950 standard; DNA; 765 BP.  
 AC ADB87950;  
 DT 04-DEC-2003 (first entry)  
 XX  
 XX Human UGT1A1 gene sequence SEQ ID NO:674.  
 DE  
 XX  
 XX Irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;  
 KM colorectal cancer; cervical cancer; gastric cancer; lung cancer;  
 KM ovarian cancer; pancreatic cancer; malignant glioma;  
 XX uridine diphosphate glycosyltransferase1 member A1; gene; ds.  
 OS  
 XX Homo sapiens.  
 XX  
 PN WO2003013536-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 23-JUL-2002; 2002WO-EP008217.  
 XX  
 PR 23-JUL-2001; 2001EP-00117608.  
 PR 24-MAY-2002; 2002EP-00011710.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Heinrich G, Kerb R;  
 XX  
 DR WPI, 2003-289896/28.  
 XX  
 XX Use of irinotecan to treat cancer patient by determining if patient has  
 PT variant alleles of UGT1A1 gene, administering increased/decreased amounts  
 PR of irinotecan based on increased/decreased levels of UGT1A1 gene product.  
 PS  
 XX Disclosure, SEQ ID NO 674; 107bp; English.  
 XX  
 XX The invention relates to the novel use of irinotecan to treat a patient  
 CC suffering from cancer. This involves determining if the patient has one  
 CC or more variant alleles of the UGT1A1 gene, and if the patient has one or  
 CC more of such variant alleles, irinotecan is administered in an increased  
 CC or decreased amount in comparison to the amount that is administered  
 CC without regard to the patient's alleles in the UGT1A1 gene. The invention  
 CC has cytostatic activity. A composition of the invention acts as a  
 CC topoisomerase I inhibitor. The method is useful for treating a patient,  
 CC an animal e.g. mouse or a human, preferably African or Asian, suffering  
 CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,  
 CC pancreatic cancer or malignant glioma. The present sequence is used in  
 CC the exemplification of the invention.  
 XX  
 XX Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;

```

Query Match      100.0%; Score 25; DB 10; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTGACATTTTCAGCGCCATAGCGAA 25
        |||||
Db      672 GTGACATTTTCAGCGCCATAGCGAA 648

RESULT 9
ADB96933/c
ID ADB96933 standard; DNA: 765 BP.
XX
XX ADB96933;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human MDR1 related DNA sequence SEQ ID NO:674.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX multidrug resistance 1; MDR1; cytosstatic; human; CYP3A5; MRP1; MDR1;
XX TOP1; ds.
XX
XX Homo sapiens.
XX
XX WO2003013537-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX
XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
XX treating cancer in subject having genome with variant allele comprising
XX multidrug resistance 1 polynucleotide.
XX
XX Disclosure; SEQ ID NO 674; 130pp; English.
XX
XX The invention relates to the novel use of irinotecan or its derivative
XX for the preparation of pharmaceutical compositions for treating
XX colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
XX malignant glioma in a subject having a genome with a variant allele which
XX comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
XX of the invention has cytosstatic activity. The invention is useful for the
XX preparation of pharmaceutical compositions for treating colorectal,
XX cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
XX glioma in a subject (preferably human, more preferably African or Asian)
XX or a mouse. The present sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;

Query Match      100.0%; Score 25; DB 10; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTGACATTTTCAGCGCCATAGCGAA 25
        |||||
Db      672 GTGACATTTTCAGCGCCATAGCGAA 648

RESULT 10
ADB92124/c
ID ADB92124 standard; DNA: 765 BP.

```

```

XX AC ADB92124;
XX DT 04-DEC-2003 (first entry)
XX DE Human MDR1 related DNA sequence SEQ ID NO:674.
XX KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX KW multidrug resistance 1; MDR1; cytosstatic; human; UGT1A1; MRP1; TOP1; ds.
XX OS Homo sapiens.
XX PN MO2003013535-A2.
XX PD 20-FEB-2003.
XX PF 23-JUL-2002; 2002MO-EP008220.
XX PR 23-JUL-2001; 2001EP-00117608.
XX PR 24-MAY-2002; 2002EP-00011710.
XX PA (EPID-) EPIDAVROS BIOTECHNOLOGIE AG.
XX PI Heinrich G, Kerb R;
XX DR WPI; 2003-342400/32.
XX PT New use of irinotecan for preparation of pharmaceutical compositions for
XX PT treating cancer in subject having genome with variant allele comprising
XX PT multidrug resistance 1 polynucleotide.
XX PS Disclosure; SEQ ID NO 674; 104bp; English.
XX CC The invention relates to a novel use of irinotecan or its derivative for
XX CC the preparation of a pharmaceutical composition for treating colorectal,
XX CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
XX CC glioma in a subject having a genome with a variant allele which comprises
XX CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
XX CC invention has cytostatic activity. The present sequence is used in the
XX CC exemplification of the invention.
XX SQ Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 10; Length 765;
XX Best Local Similarity 100.0%; Pred. No. 0.026;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 672 GTGACATTTTCACGGCCATAGCGAA 648

```

RESULT 11  
AB565230/C  
ID AB565230 standard; cDNA; 2307 BP.  
XX  
XX AB565230;  
XX  
XX 15-NOV-2002 (first entry)  
XX  
XX cDNA encoding tumour involved gene (TIG) splice variant, NV-31.  
XX  
XX Human, 66; gene; splice variant; tumour-involved gene; TIG;  
XX KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;  
XX KW endothelial cell; cell differentiation; cell proliferation; apoptosis;  
XX KW gene therapy.  
XX  
XX OS Homo sapiens.  
XX PN US2002086384-A1.  
XX PD 04-JUL-2002.

```

XX PF 13-MAR-2001; 2001US-00805020.
XX PR 14-MAR-2000; 2000IL-00135402.
XX PR 16-MAY-2000; 2000IL-00136154.
XX PA (LEVI/) LEVINE Z.
XX PA (DAVI/) DAVID A.
XX PA (ROMA/) ROMANO C.
XX PA (BERN/) BERNSTEIN J.
XX PI Levine Z, David A, Romano C, Bernstein J;
XX PN WPI; 2002-635679/68.
XX DR P-PSDB; ABG79700.
XX PF Novel nucleic acid sequence, which is an alternative splicing variant of
XX PF tumor involved genes, useful for detecting cancer, predisposition to
XX PF cancer, for evaluating cancer state and in gene therapy for treating
XX PF cancer.
XX PS Claim 1; Page 60-61; 180bp; English.
XX CC The invention discloses isolated human nucleic acid alternative splicing
XX CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
XX CC polypeptides are useful for determining the level of a nucleic acid or
XX CC polypeptide in a biological sample, for detecting a variant nucleic acid
XX CC or polypeptide sequence in a biological sample, for determining the level
XX CC of variant nucleic acid or polypeptide sequences in a biological sample
XX CC and for determining the ratio between the level of variant sequence in a
XX CC first biological sample and the level of the original sequence from which
XX CC the variant has been varied by alternative splicing in a second
XX CC biological sample and for raising antibodies. A pharmaceutical
XX CC composition comprising a carrier and the nucleic acid, is useful for
XX CC treating diseases (e.g. cancer) that can be ameliorated or cured by
XX CC increasing or decreasing the level of the encoded protein. The nucleic
XX CC acids are also useful for diagnostic purposes, especially for detecting
XX CC cancer or a predisposition to cancer, for evaluating the state or
XX CC aggressiveness of cancer disease, in basic research, for understanding
XX CC the physiological function of the original TIG, in targeting or
XX CC developing pharmaceuticals, for distinguishing various stages in the life
XX CC cycle of the same type of cells which may be helpful for the development
XX CC of pharmaceuticals for various cancer stages in which cell cycle is non-
XX CC normal, for determining mutations in tumour-involved genes and in gene
XX CC therapy. The polypeptides are useful for identifying compounds capable of
XX CC binding to the variant product and modulating its activity and for
XX CC modulating apoptosis either ex vivo or in vivo. The sequences presented in
XX CC AB5652200-AB565235 are the coding sequences for the new variants (NV) 1-
XX CC 36 of the TIGs disclosed
XX SQ Sequence 2307 BP; 662 A; 441 C; 591 G; 612 T; 0 U; 1 Other;
XX
XX Query Match 100.0%; Score 25; DB 6; Length 2307;
XX Best Local Similarity 100.0%; Pred. No. 0.032;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1911 GTGACATTTTCACGGCCATAGCGAA 1887

```

RESULT 12  
ABV78146/C  
ID ABV78146 standard; DNA; 3840 BP.  
XX  
XX ABV78146;  
XX  
XX 15-NOV-2002 (first entry)  
XX  
XX Human mdr-1 DNA SEQ ID NO 30.  
XX  
XX RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytosstatic;

Accession	Sequence	Score	DB	Length
09-JAN-2001; 2001DE-01000588.				
(RIBO-) RIBOPHARMA AG.				
Kreutzler R, Limmer S, Rost S, Hadwiger P;				
WPI; 2002-683450/74.				
Claim 13; Page 27-28; 100pp; German.				
The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNA and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention				
Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;				
Query Match	100.0%;	Score 25;	DB 6;	Length 3840;
Best Local Similarity	100.0%;	Pred. No. 0.036;		
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
1 GTGACATTTTCACGGCCATACGAA 25				
1484 GTGACATTTTCACGGCCATACGAA 1460				
RESULT 14				
ABX09965/c				
ID ABX09965 standard; DNA; 3840 BP.				
AC				
ABX09965;				
23-JAN-2003 (first entry)				
Human mdr-1 DNA fragment SEQ ID 30.				
Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;				
prion; inhibition; human; ds.				
Homo sapiens.				
DE10100587-C1.				
21-NOV-2002.				
09-JAN-2001; 2001DE-01000587.				
09-JAN-2001; 2001DE-01000587.				
(RIBO-) RIBOPHARMA AG.				
Kreutzler R, Limmer S, Rost S, Hadwiger P;				
WPI; 2002-742209/81.				
Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon				

XX Disclosure; Page 32-33; 98pp; German.  
 PS  
 CC This invention describes a novel method for inhibiting expression of a  
 CC target gene by introducing into the cell that contains the target gene at  
 CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)  
 CC structure of not more than 49 consecutive nucleotides (nt), where at  
 CC least a segment of one strand of the ds structure is complementary with  
 CC the target gene and the cells are treated with interferon before  
 CC introduction of dsRNA. The method is used to inhibit expression of  
 CC target genes, particularly oncogenes, cytokine genes, Id (not defined)  
 CC protein genes; developmental or prion genes, or genes expressed in  
 CC pathogenic organisms (particularly plasmodia) or in viruses or viroids  
 CC (pathogenic in humans, animals or plants). Treating the cells with  
 CC interferon greatly increases the extent to which dsRNA can inhibit  
 CC expression of the target genes, and the effect is even greater when dsRNA  
 CC are modified to increase their stability. ABX0936-ABX10075 represent  
 CC gene fragments used to illustrate the method of the invention  
 XX  
 SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 6; Length 3840;  
 Best Local Similarity 100.0%; Pred. No. 0.036;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GTGACATTTTCACGGCCATAGCGAA 25  
 Db 1484 GTGACATTTTCACGGCCATAGCGAA 1460  
 RESULT 15  
 ABL91687/C  
 ID ABL91687 standard; DNA; 3840 BP.  
 AC ABL91687;  
 XX  
 DT 28-MAY-2002 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 30.  
 XX  
 KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;  
 KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;  
 KW cytosstatic; virucide; protozoacide; antibacterial; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE10100586-C1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 09-JAN-2001; 2001DE-01000586.  
 XX  
 PR 09-JAN-2001; 2001DE-01000586.  
 XX  
 PA (RIBO-) RIBOPHARMA AG.  
 XX  
 PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
 XX  
 DR WPI; 2002-270454/32.  
 XX  
 PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by  
 PT introducing double-stranded complementary oligoRNA having unpaired  
 PT terminal bases.  
 XX  
 PS Claim 13; Page 28-30; 104pp; German.  
 CC  
 CC The invention relates to a method for inhibiting expression of a target  
 CC gene (ABL91688-ABL91797) in a cell by introducing at least one  
 CC oligoribonucleotide that has a double-stranded structure consisting of at  
 CC most 49 sequential nucleotide pairs, with at least part of one strand  
 CC complementary with the target gene and has at least one end a single-  
 CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for  
 CC antisense inhibition of gene expression useful e.g. for treating tumours

CC but the oligoribonucleotides may also be directed against genes present  
 CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,  
 CC animals or plants) or against cytokine, Id, developmental or prion genes.  
 CC The method provides more effective inhibition of gene expression than use  
 CC of known oligonucleotides, probably because the unpaired overhang  
 CC increases stability and thus intracellular concentration  
 XX  
 SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 6; Length 3840;  
 Best Local Similarity 100.0%; Pred. No. 0.036;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1484 GTGACATTTTCACGGCCATAGCGAA 1460  
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 Job time : 245.69 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using -sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds  
(without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 25

Sequence: 1 ggcagatttcacggccatcagcgaa 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	25	100.0	219	16	US-10-029-386-15991
2	25	100.0	584	16	US-10-029-386-2291
3	25	100.0	2307	9	US-09-805-020-31
4	25	100.0	3840	18	US-10-384-033C-10
5	25	100.0	3860	9	US-09-866-866A-1
6	25	100.0	3860	9	US-09-866-866A-3
7	25	100.0	4533	9	US-09-805-020-30
8	25	100.0	4643	13	US-10-072-621-2
9	25	100.0	4643	14	US-10-097-340-1
10	25	100.0	4643	15	US-10-007-925A-258
11	25	100.0	4646	11	US-09-968-007A-459

c 12	25	100.0	4646	11	US-09-968-007A-747	Sequence 747, App
c 13	25	100.0	4646	17	US-10-641-641-1167	Sequence 1167, App
c 14	25	100.0	4646	17	US-10-343-657-1	Sequence 1, Appl1
c 15	25	100.0	4646	18	US-10-775-169-198	Sequence 198, App
c 16	25	100.0	4669	18	US-10-680-516-1	Sequence 1, Appl1
c 17	25	100.0	8630	9	US-09-306-417-1	Sequence 1, Appl1
c 18	25	100.0	8630	9	US-09-306-417-2	Sequence 2, Appl1
c 19	23.4	93.6	4317	13	US-10-044-671-1	Sequence 1, Appl1
c 20	23.4	93.6	4317	18	US-10-896-434-1	Sequence 1, Appl1
c 21	21.8	87.2	3852	17	US-10-101-433A-1	Sequence 1, Appl1
c 22	21.8	87.2	4186	15	US-10-619-359A-1	Sequence 1, Appl1
c 23	21.8	87.2	4189	9	US-09-866-866A-5	Sequence 5, Appl1
c 24	21.8	87.2	4195	17	US-10-619-359A-3	Sequence 3, Appl1
c 25	21.8	87.2	4254	17	US-09-917-800A-1424	Sequence 1424, App
c 26	21.8	87.2	4254	17	US-10-398-934-265	Sequence 265, App
c 27	21.8	87.2	4254	17	US-10-152-319A-1464	Sequence 1464, App
c 28	21.8	87.2	4298	18	US-10-335-053-32	Sequence 32, Appl
c 29	21.8	87.2	4369	9	US-09-769-097-1	Sequence 1, Appl1
c 30	21.8	87.2	4425	9	US-09-769-097-3	Sequence 3, Appl1
c 31	21.8	87.2	4788	9	US-09-866-866A-7	Sequence 7, Appl1
c 32	19	76.0	398	18	US-10-357-930-11474	Sequence 11474, A
c 33	19	76.0	416	18	US-10-357-930-2305	Sequence 2305, App
c 34	19	76.0	490	15	US-10-102-524-430	Sequence 430, App
c 35	19	76.0	539	18	US-10-357-930-32646	Sequence 32646, A
c 36	19	76.0	539	18	US-10-357-930-41572	Sequence 41572, A
c 37	19	76.0	582	15	US-10-102-524-344	Sequence 344, App
c 38	19	76.0	2807	14	US-10-097-340-56	Sequence 56, Appl
c 39	19	76.0	2807	15	US-10-177-293-75	Sequence 75, Appl
c 40	19	76.0	3321	9	US-09-825-294-175	Sequence 175, App
c 41	19	76.0	3321	9	US-09-880-107-2253	Sequence 2253, App
c 42	19	76.0	3321	9	US-09-970-966-175	Sequence 175, App
c 43	19	76.0	3321	14	US-10-076-816-50	Sequence 50, Appl
c 44	19	76.0	3321	14	US-10-097-340-58	Sequence 58, Appl
c 45	19	76.0	3321	15	US-10-177-293-77	Sequence 77, Appl

## ALIGNMENTS

RESULT 1  
US-10-029-386-15991  
Sequence 15991, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEOMITC-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 15991  
LENGTH: 219  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR7.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6  
OTHER INFORMATION: NT HIT: M29432.1, EVALUE 1.00e-120  
OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 8.00e-33  
OTHER INFORMATION: EST\_HUMAN HIT: BG567305.1, EVALUE 1.10e+00  
US-10-029-386-15991  
Query Match 100.0%; Score 25; DB 16; Length 219;  
Best local similarity 100.0%; Pred. No. 0.016;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
DB 77 GTGACATTTTCACGGCCATAGCGAA 101

RESULT 2  
US-10-029-386-2291  
; Sequence 2291, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: ABOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 2291  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR7,1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6  
; OTHER INFORMATION: NT HIT: M29432.1, EVALUE 0.00e+00  
US-10-029-386-2291

Query Match 100.0%; Score 25; DB 16; Length 584;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
DB 320 GTGACATTTTCACGGCCATAGCGAA 344

RESULT 3  
US-09-805-020-31/C  
; Sequence 31, Application US/09805020  
; Publication No. US20020086384A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Zurlic  
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES  
; FILE REFERENCE: 2786-0168P  
; CURRENT APPLICATION NUMBER: US/09/805,020  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(2307)  
; OTHER INFORMATION: any n = a,c,g,t any unknown or other  
US-09-805-020-31

Query Match 100.0%; Score 25; DB 9; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||

DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 4  
US-10-384-339C-30/C  
; Sequence 30, Application US/10384339C  
; Publication No. US20040175703A1  
; GENERAL INFORMATION:  
; APPLICANT: Kretzler, Roland  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GEN  
; FILE REFERENCE: 20200/2002  
; CURRENT APPLICATION NUMBER: US/10/384,339C  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: DE 10100586.5  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: DE 10155280.7  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: DE 10158411.3  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: DE 10160151.4  
; PRIOR FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 3840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; TITLE: mdr-1  
; PATENT DOCUMENT NUMBER: AFO16535  
US-10-384-339C-30

Query Match 100.0%; Score 25; DB 18; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
DB 1484 GTGACATTTTCACGGCCATAGCGAA 1460

RESULT 5  
US-09-866-866A-1/C  
; Sequence 1, Application US/09866866A  
; Patent No. US20020102244A1  
; GENERAL INFORMATION:  
; APPLICANT: Sorrentino, Brian  
; APPLICANT: Schuetz, John  
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
; FILE REFERENCE: 1340-1-021CIP2  
; CURRENT APPLICATION NUMBER: US/09/866,866A  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 09/584,586  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: PCT/US99/11825  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: 60/086,988  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3860  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||

Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463

## RESULT 6

US-09-866-866A-3/C  
Sequence 3, Application US/09866866A  
Patent No. US2002010224A1  
GENERAL INFORMATION:  
APPLICANT: Schuetz, John  
APPLICANT: Sorrentino, Brian  
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
FILE REFERENCE: 1340-1-022CIP2  
CURRENT APPLICATION NUMBER: US/09/866,866A  
CURRENT FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: 09/584,586  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: PCT/US99/11825  
PRIOR FILING DATE: 1999-05-27  
PRIOR APPLICATION NUMBER: 60/086,988  
PRIOR FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 3860  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-866-866A-3

Query Match 100.0%; Score 25; DB 9; Length 3860;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25  
Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463

## RESULT 7

US-09-805-020-30/C  
Sequence 30, Application US/09805020  
Publication No. US20020086384A1  
GENERAL INFORMATION:  
APPLICANT: Levine, Zuzit  
TITLE OF INVENTION: SPICE VARIANTS OF ONCOGENES  
FILE REFERENCE: 2786-0168P  
CURRENT APPLICATION NUMBER: US/09/805,020  
CURRENT FILING DATE: 2001-03-13  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 4533  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)-(4533)  
OTHER INFORMATION: any n = a,c,g,t any unknown or other  
US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25  
Db 1911 GTGACATTTTCACGGCCATAGCGAA 1887

## RESULT 8

US-10-072-621-2/C  
Sequence 2, Application US/10072621  
Publication No. US20020169137A1

GENERAL INFORMATION:  
APPLICANT: Reiner, Peter B.  
APPLICANT: Connor, Bruce P.  
APPLICANT: Pollard, Michelle  
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION  
FILE REFERENCE: 100103.402  
CURRENT APPLICATION NUMBER: US/10/072,621  
CURRENT FILING DATE: 2002-02-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 4643  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25  
Db 1908 GTGACATTTTCACGGCCATAGCGAA 1884

## RESULT 9

US-10-097-340-1/C  
Sequence 1, Application US/10097340  
Publication No. US2003008750A1  
GENERAL INFORMATION:  
APPLICANT: John MONAHAN  
APPLICANT: Manjula GANNAPARAPU  
APPLICANT: Sebastian HOERSCH  
APPLICANT: Shubhangi KAWATKAR  
APPLICANT: Steve G. KOVATS  
APPLICANT: Rachel E. MEYERS  
APPLICANT: Michael MORRISSEY  
APPLICANT: Peter OLANDT  
APPLICANT: Ami SEN  
APPLICANT: Peter VEIBY  
APPLICANT: Gordon B. MILLS  
APPLICANT: Robert C. BAST, Jr.  
APPLICANT: Karen LU  
APPLICANT: Rosemarie SCHMANT  
APPLICANT: Xumei ZHAO  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Title Of Invention: Assessment, Prevention, and Therapy of Ovarian Cancer  
FILE REFERENCE: MRI-030  
CURRENT APPLICATION NUMBER: US/10/097,340  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 60/276,025  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/325,149  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/276,026  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/324,967  
PRIOR FILING DATE: 2001/09/26  
PRIOR APPLICATION NUMBER: 60/311,732  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/325,102  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/323,580  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 363  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 4643  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-097-340-1

Query Match 100.0%; Score 25; DB 14; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1908 GTGACATTTTCACGGCCATAGCGAA 1884

RESULT 10  
US-10-007-926A-258/c  
Sequence 258, Application US/10007926A  
Publication No. US20030143539A1  
GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCOIS  
APPLICANT: HOUIGATTE, RENI  
APPLICANT: BIRNBAUM, DANIEL  
APPLICANT: NGUYEN, CATHERINE  
APPLICANT: VIENS, PATRICE  
APPLICANT: FEET, VINCENT  
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS  
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES  
FILE REFERENCE: 1546-R-00  
CURRENT APPLICATION NUMBER: US/10/007,926A  
CURRENT FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 60/254,090  
PRIOR FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 258  
LENGTH: 4643  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

OTHER INFORMATION: acp-binding cassette, sub-family b  
OTHER INFORMATION: (mdr/cap, member 1 (ABCB1) gene.  
US-10-007-926A-258

Query Match 100.0%; Score 25; DB 15; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1908 GTGACATTTTCACGGCCATAGCGAA 1884

RESULT 11  
US-09-968-007A-459/c  
Sequence 459, Application US/09968007A  
Publication No. US20040115625A1  
GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa  
FILE REFERENCE: 689290-71  
CURRENT APPLICATION NUMBER: US/09/968,007A  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,172  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,173  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,278  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,294  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,295  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,316  
NUMBER OF SEQ ID NOS: 1001  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 459  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-968-007A-459

Query Match 100.0%; Score 25; DB 11; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 12  
US-09-968-007A-747/c  
Sequence 747, Application US/09968007A  
Publication No. US20040115625A1  
GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat  
TITLE OF INVENTION: Gene Sets  
FILE REFERENCE: 689290-71  
CURRENT APPLICATION NUMBER: US/09/968,007A  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,172  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,173  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,278  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,294  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,295  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,316  
NUMBER OF SEQ ID NOS: 1001  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 747  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-968-007A-747

Query Match 100.0%; Score 25; DB 11; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25  
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 13  
US-10-641-643-1167/c  
Sequence 1167, Application US/10641643  
Publication No. US20040077003A1  
GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.  
Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304



COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/641,643  
 FILING DATE: 14-Aug-2003  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: <Unknown>  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 1167:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4646 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: 9187468  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :  
 US-10-641-643-1167

Query Match 100.0%; Score 25; DB 17; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.028;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
 DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 14  
 US-10-343-657-1/c  
 ; Sequence 1, Application US/10343657  
 ; Publication No. US2004008682A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruth, Adam  
 ; APPLICANT: Roninson, Igor B.  
 ; TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its  
 ; FILE REFERENCE: 00,616-A  
 ; TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs  
 ; CURRENT APPLICATION NUMBER: US/10/343,657  
 ; CURRENT FILING DATE: 2003-10-17  
 ; PRIOR APPLICATION NUMBER: 60/222,313  
 ; PRIOR FILING DATE: 2000-08-01  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4646  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (425)..(4264)  
 US-10-343-657-1

Query Match 100.0%; Score 25; DB 17; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.028;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
 DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 15

US-10-775-169-198/c  
 ; Sequence 198, Application US/10775169  
 ; Publication No. US20040175743A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Burczynski, Michael  
 ; APPLICANT: Twine, Natalie  
 ; APPLICANT: Dornier, Andrew  
 ; APPLICANT: Trepicchio, William  
 ; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
 ; FILE REFERENCE: AM101080 (031896-013000)  
 ; CURRENT APPLICATION NUMBER: US/10/775,169  
 ; CURRENT FILING DATE: 2004-02-11  
 ; NUMBER OF SEQ ID NOS: 5278  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 198  
 ; LENGTH: 4646  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-775-169-198

Query Match 100.0%; Score 25; DB 18; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.028;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
 DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

Search completed: February 9, 2005, 22:26:40  
 Job time : 267.667 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds  
(without alignments)  
388.593 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 25

Sequence: 1 gtgacatttcacggccatgacgaa 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	570	5	BP220580 BP220580
2	25	100.0	3843	9	AY408954 Homo sapi
3	25	100.0	3843	9	AY408955 Pan trogl
4	23.4	93.6	929	5	BO882401 AGENCOURT
5	21.8	87.2	485	5	CB727009 AMGNNUC:N
6	21.8	87.2	784	4	B1184814 UNL-P-FN-
7	21.8	87.2	894	4	BF584668 602098406
8	21.8	87.2	3182	3	AK030328 Mus muscu
9	21.8	87.2	3816	9	AY408956 Mus muscu
10	20.2	80.8	411	9	CL388323 RPI14.28
11	20.2	80.8	674	5	BU437349 604145718
12	20.2	80.8	716	5	BU239912 603322470
13	19.8	79.2	578	5	BP261688 BP261688
14	19.8	79.2	923	6	CD251708 AGENCOURT
15	19.8	79.2	1235	4	BM542792 AGENCOURT
16	19.2	76.8	422	1	AG654223 AG654223
17	19.2	76.8	448	6	CA780376 MP384.6
18	19.2	76.8	463	5	BY431405 BY431405
19	19.2	76.8	535	5	BK678520 BK678520
20	19.2	76.8	582	5	BP193611 BP193611
21	19.2	76.8	588	7	CF359931 821214 MA
22	19.2	76.8	604	7	CK459590 929792 MA
23	19.2	76.8	608	2	BE291003 601084181
24	19.2	76.8	665	7	CN157996 946753 MA

C 25	19.2	76.8	665	7	CN159932	949057 MA
C 26	19.2	76.8	672	4	BI092416	BI092416 602856993
C 27	19.2	76.8	710	7	CK460832	CK460832 9311149 MA
C 28	19.2	76.8	730	7	CK460130	CK460130 930381 MA
C 29	19.2	76.8	772	4	BG915267	BG915267 602814579
C 30	19.2	76.8	831	4	BI660209	BI660209 603302136
C 31	19.2	76.8	852	4	BI181199	BI181199 UNL-P-FN-
C 32	19.2	76.8	858	2	BE913573	BE913573 601667516
C 33	19.2	76.8	904	4	BI661427	BI661427 60304721
C 34	19.2	76.8	984	4	BI409869	BI409869 602962207
C 35	19.2	76.8	333	1	AI524590	AI524590 t043f08.x
C 36	19.2	76.0	366	1	BM856196	BM856196 K-BEST0139
C 37	19.2	76.0	371	1	AV695293	AV695293 AV695293
C 38	19.2	76.0	405	1	AI921934	AI921934 wmb6h05.x
C 39	19.2	76.0	411	8	AO194986	AO194986 RPI11-57
C 40	19.2	76.0	421	4	BM719759	BM719759 UI-E-EJ1-
C 41	19.2	76.0	426	4	BM684114	BM684114 UI-E-EJ1-
C 42	19.2	76.0	429	8	AO194770	AO194770 RPI11-57
C 43	19.2	76.0	434	1	AV648804	AV648804 AV648804
C 44	19.2	76.0	481	5	BO028054	BO028054 UI-H-CO-
C 45	19.2	76.0	501	1	AU149941	AU149941 AU149941

## ALIGNMENTS

RESULT 1	BP220580/c	570 bp	mRNA	linear	EST 15-SEP-2004
LOCUS	BP220580	Sugano cDNA library, colon	Homo sapiens	cDNA clone	
DEFINITION	COL03695, mRNA sequence.				
ACCESSION	BP220580				
VERSION	BP220580.1	GI:52093485			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 570)				
AUTHORS	Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.				
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions				
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)				
COMMENT	Contact: Yutaka Suzuki Department of Medical Science, University of Tokyo Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.				
FEATURES	source	location/Qualifiers			
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		/mol_type="mRNA"			
		/db_xref="taxon:9606"			
		/clone="COL03695"			
		/issue_type="colon"			
		/clone_lib="Sugano cDNA library, colon"			
ORIGIN					
Query Match	100.0%	Score 25; DB 5; Length 570;			
Best Local Similarity	100.0%	Pred. No. 0.25;			
Matches	25; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Qy	1	GTGACATTTTCACGGCCATAGCGAA	25		
Db	92	GTGACATTTTCACGGCCATAGCGAA	68		
RESULT 2	AY408954/c	3843 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY408954	Homo sapiens ABCB1 gene, VIRTUAL TRANSCRIPT, partial			
DEFINITION	genomic survey sequence.				

ACCESSION AY408954  
VERSION AY408954.1 GI:39764922  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3843)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 3843)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..3843  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>3843  
/gene="ABCB1"  
/locus\_tag="HCM3396"  
ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463  
1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
1487 GTGACATTTTCACGGCCATAGCGAA 1463  
RESULT 3  
AY408955/c  
LOCUS AY408955 3843 bp DNA linear GSS 15-DEC-2003  
DEFINITION Pan troglodytes ABCB1 gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY408955  
VERSION AY408955.1 GI:39764923  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1 (bases 1 to 3843)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 3843)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..3843  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>3843  
/gene="ABCB1"  
/locus\_tag="HCM3396"  
ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463  
1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
1487 GTGACATTTTCACGGCCATAGCGAA 1463  
RESULT 4  
BQ882401/c  
LOCUS BQ882401 929 bp mRNA linear EST 16-AUG-2002  
DEFINITION AGENCOURT 8627902 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:6291782  
5', mRNA sequence.  
ACCESSION BQ882401  
VERSION BQ882401.1 GI:22274409  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 929)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: ggaaps-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LINC2492 row: c column: 15  
High quality sequence stop: 677.  
FEATURES  
source  
1..929  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6291782"  
/issue\_type="normal pigmented retinal epithelium"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_43"  
/note="Organ: eye; Vector: pOTB7, Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library. |"  
ORIGIN  
Query Match 93.6%; Score 23.4; DB 5; Length 929;  
Best Local Similarity 96.0%; Pred. No. 1.7;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 GTGACATTTTCACGGCCATAGCGAA 25

Db 753 GTGACATTTTCAGCGCCATAGCGAA 729

RESULT 5 CB8727009/c 485 bp mRNA linear EST 11-APR-2003

LOCUS AMONNC:NRHYS-00278-B7-A w Rat hypothalamus (10471) Rattus  
DEFINITION norvegicus cDNA clone nrhys-00278-b7 5', mRNA sequence.

ACCESSION CB8727009 GI:29793993

VERSION EST.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 485)

AUTHORS Amgen EST Program.

TITLE Amgen Rat EST Program

JOURNAL Unpublished (2003)

COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00278 row: b column: 7.

FEATURES 1..485  
source location/Qualifiers

/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="nrhys-00278-b7"  
/clone\_lib="w Rat hypothalamus (10471)"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; w Rat  
hypothalamus adult female Wistar rat avg. insert size 2.3  
kb fraction 6 and 7"

ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 485;  
Best Local Similarity 92.0%; Pred. No. 9.5;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCAGCGCCATAGCGAA 25

Db 239 GTGACGTTTTCGCGCCATAGCGAA 215

RESULT 6 B1184814 784 bp mRNA linear EST 10-JUL-2001  
LOCUS UNL-P-FN-cr-g-09-0-UNL.61 UNL-P-FN Sus scrofa cDNA clone  
DEFINITION UNL-P-FN-cr-g-09-0-UNL 3', mRNA sequence.

ACCESSION B1184814 GI:14659223

VERSION EST.

KEYWORDS Sus scrofa (pig)

SOURCE Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 784)

AUTHORS Caetano, A.R., Johnson, R.K. and Pomp, D.

TITLE Generation and sequence characterization of a normalized cDNA  
library from swine ovarian follicles

JOURNAL Mamm. Genome 14 (1), 65-70 (2003)

MEDLINE 22419904

COMMENT Contact: Pomp, D  
Department of Animal Science  
University of Nebraska, Lincoln  
Lincoln, NE 68583-0908, USA  
Tel: 402 472 6416  
Fax: 402 472 6362  
Email: dpomp@unl.edu

Oligo-dT track not found, Not I site shown in beginning of sequence  
is likely internal to the message.  
Seq primer: M13 -29  
POLYA=No.

FEATURES 1..784  
source location/Qualifiers

/organism="Sus scrofa"  
/mol\_type="mRNA"  
/strain="University of Nebraska, Lincoln Swine Selection  
Lines"  
/db\_xref="taxon:9823"  
/clone="UNL-P-FN-cr-g-09-0-UNL"  
/dev\_stage="ADULT"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UNL-P-FN"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The UNL-P-FN  
library is a normalized library representing porcine  
ovarian follicles, ranging between 2.0 to 10.0 mm in  
diameter, collected during 7 days of the follicular phase  
of the pig estrous cycle. This library was derived from  
the library UNL-P-F2. The tag is a string of 5-6  
nucleotides present between the Not I site and the  
oligo-dT track. The library was constructed as described  
by Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996.  
TAG\_SEQ=None found"

ORIGIN

Query Match 87.2%; Score 21.8; DB 4; Length 784;  
Best Local Similarity 92.0%; Pred. No. 10;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCAGCGCCATAGCGAA 25

Db 201 GTGACATTTTCGCGCCATAGCGAA 225

RESULT 7 BF584668 894 bp mRNA linear EST 12-DEC-2000  
LOCUS 602098406F1 NCI CGAP\_Co24 Mus musculus cDNA clone IMAGE:421835 5',  
DEFINITION mRNA sequence.

ACCESSION BF584668

VERSION EST.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 894)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contract: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: L1A9798 row: 1 column: 02  
High quality sequence stop: 651.

FEATURES 1..894  
source location/Qualifiers

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4218385"  
/lab\_host="DH10B (T1 phage-resistant)"

## ORIGIN

/clone.lib="NCI CGAP Co24"  
 /note="Organ: Clonon; Vector: pCMV-SPORT6; Site: 1; NotI;  
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI CGAP Library."

## Query Match

Best Local Similarity 92.0%; Pred. No. 11;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## Qy

1 GTGACATTTTCAGCGCCATAGCGAA 25  
 491 GTGACATCTTCTCGGCATAGCGAA 467

## Db

RESULT 8  
 AK030328/c 3182 bp mRNA linear HTC 03-APR-2004  
 LOCUS  
 DEFINITION  
 Mus musculus 11 days pregnant adult female ovary and uterus cDNA,  
 RIKEN full-length enriched library, clone:5031438E12  
 product:ARP-binding cassette, sub-family B (MDR/TRAP), member 1B,  
 full insert sequence.

## ACCESSION

AK030328  
 AK030328.1 GI:26081769

## VERSION

HTC; CAP trapper.

## KEYWORDS

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

1

Carninci, P., and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Kono, H., Akiyama, Y., Nishi, K., Kikunaka, T., Tashiro, H., Itoh, M.,

Sun, N., Ishii, Y., Nakamura, S., Hazama, S., Nishino, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The PANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analyses of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3182)

Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

## TITLE

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Kahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M., and Hayashizaki, Y.

## JOURNAL

Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.

## FEATURES

## source

1..3182

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="PANTOM:DB:5031438E12"

/db\_xref="taxon:10090"

/clone="5031438E12"

/sex="female"

/tissue\_type="ovary and uterus"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="11 days pregnant adult"

1..3182

/note="ARP-binding cassette, sub-family B (MDR/TRAP),  
 member 1B (MGI:97568, GBI:NM\_011075, evidence: BLASTN,  
 99%, match=2587)"

99%, match=2587"

## ORIGIN

Query Match 87.2%; Score 21.8; DB 3; Length 3182;  
 Best Local Similarity 92.0%; Pred. No. 14;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## Qy

1 GTGACATTTTCAGCGCCATAGCGAA 25  
 1576 GTGACATCTTCTCGGCATAGCGAA 1552

## Db

## RESULT 9

AY408956/c

LOCUS

DEFINITION

Mus musculus ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

AY408956

ACCESSION

AY408956.1 GI:39764924

VERSION

KEYWORDS

GSS.

SOURCE

Mus musculus

(house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3816)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Perletera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 3816)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source  
1..3816  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/gene="ABCB1"  
/locus\_tag="HMC3396"

ORIGIN

Query Match 87.2% Score 21.8; DB 9; Length 3816;  
Best Local Similarity 92.0%; Pred. No. 14;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
1475 GTGACATTTTCGCGCCATAGCGAA 1451

Db

RESULT 10

LOCUS CL388323 411 bp DNA linear GSS 19-AUG-2004

DEFINITION RPCR144\_284D11.r RPCR1-44 Sus scrofa genomic clone RPCR144\_284D11, genomic survey sequence.

ACCESSION CL388323

VERSION CL388323.1 GI:51440283

KEYWORDS GSS.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthera; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 411)  
Rogatcheva, M.B., Meyers, S., He, W., Larkin, D.M., Marron, B.M., Beaver, J.E. and Schock, L.B.  
Piggy-BACing the Human Genome: Constructing a Porcine Physical Map Through Comparative Genomics  
Unpublished (2004)

TITLE Through Comparative Genomics

JOURNAL Unpublished (2004)

COMMENT Other GSSes: RPCR144\_284D11.f  
Contact: Lawrence B. Schock  
Department of Animal Sciences  
University of Illinois at Urbana Champaign  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 265 5326  
Fax: 217 244 5617  
Email: schock@uiuc.edu  
Clones are derived from the porcine BAC library RPCR-44 (<http://www.bacpac.chori.org/porcine242.htm>). For BAC library availability, please contact Pieter de Jong ([pdejong@chori.org](mailto:pdejong@chori.org)). Clones may be purchased from BACPAC Resources (<http://BACPACresources.chori.org>). This work was undertaken as part of the International Swine Genome Sequencing Consortium by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG2002-34480-11828 from USDA-CSREES and AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing Initiative)  
Plate: 284 row: D column: 11  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source  
1..411  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/strain="four pigs (bred: 37.5% Yorks Landrace and 25% Meishan)"

/db\_xref="taxon:9823"  
/clone="RPCR144\_284D11"  
/sex="male"  
/cell\_type="blood"  
/clone\_1ib="RPCR-44"  
/note="Vector: pPARBAC2; site\_1: EcoRI; site\_2: EcoRI; porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match 80.8% Score 20.2; DB 9; Length 411;  
Best Local Similarity 88.0%; Pred. No. 57;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25  
|||||  
271 GTGACATTTTCACGGCCATAGCGAA 295

Db

RESULT 11

LOCUS BU437349/c 674 bp mRNA linear EST 29-NOV-2002

DEFINITION 604145918P1 CSEQRBN11 Gallus gallus CDNA clone CHEST986c5 5', mRNA sequence.

ACCESSION BU437349

VERSION BU437349.1 GI:25926660

KEYWORDS EST

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.  
1 (bases 1 to 674)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
2235534  
12445392

REFERENCE 1 (bases 1 to 674)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
2235534  
12445392

TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..674  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST986c5"  
/sex="Male and female"  
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/clone\_1ib="CSEQRBN11"  
/note="Vector: pBluescript II KS(+); site\_1: EcoRI; site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 674;  
 Best Local Similarity 88.0%; Pred. No. 63;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATACGGA 25  
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 DB 237 GTGACATCTCTACGGCCATACGGA 213

RESULT 12  
 BU239912/c 716 bp mRNA linear EST 26-NOV-2002  
 LOCUS 603322470F1 CSEQCHN33 Gallus gallus cDNA clone CHEST250K17 5', mRNA  
 DEFINITION sequence.

ACCESSION BU239912.1 GI:25485977  
 VERSION BU239912  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianidae; Gallus.

REFERENCE 1 (bases 1 to 716)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,  
 A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
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 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
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 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:9031"  
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 /sex="Female"  
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 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN33"  
 /note="Organ: liver; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dt) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was bluntend, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

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Qy 1 GTGACATTTTCACGGCCATACGGA 25  
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 DB 506 GTGACATCTCTACGGCCATACGGA 482

RESULT 13  
 BP261688/c 578 bp mRNA linear EST 16-SEP-2004  
 LOCUS BP261688 Sugano cDNA library, small intestine Homo sapiens cDNA  
 DEFINITION clone HS104571, mRNA sequence.

ACCESSION BP261688  
 VERSION BP261688.1 GI:52176919  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 578)  
 Suzuki, Y., Yamashita, R., Shirota, M., Sakibara, Y., Chiba, J.,  
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.,  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 Genome Res. 14 (9), 1711-1718 (2004)  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.

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 source location/Qualifiers  
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 /db\_xref="taxon:9606"  
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## ORIGIN

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 Best Local Similarity 91.3%; Pred. No. 97;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGACATTTTCACGGCCATACGGA 24  
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 DB 545 TGACATTTTCACGGCCATACGGA 523

RESULT 14  
 CD251708/c 923 bp mRNA linear EST 22-MAY-2003  
 LOCUS CD251708  
 DEFINITION AGENCOURT\_14205957 NIH\_MGC\_179 Homo sapiens cDNA clone  
 IMAGE:30384175 5', mRNA sequence.

ACCESSION CD251708  
 VERSION CD251708.1 GI:31012174  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 923)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: g9apbs@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: NDAM49 row: d column: 08  
 High quality sequence start: 2



FEATURES High quality sequence stop: 463.  
Location/Qualifiers

1. .923  
/organism="Homo sapiens"  
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/clone\_1lb="NIH\_MGC\_179"  
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 79.2%; Score 19.8; DB 6; Length 923;  
Best Local Similarity 91.3%; Pred. No. 1.1e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACATTTTCAGCGCATAGCGA 24  
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DB 580 TGACATTTTCAGCGCATAGCGA 558

RESULT 15  
BM542792 1235 bp rRNA linear EST 20-FEB-2002

LOCUS AGENCOURT\_6426041 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5520790  
DEFINITION 5', mRNA sequence.

ACCESSION BM542792

VERSION BM542792.1 GI:18772622

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE NIH-MGC http://mhc.ncl.nih.gov/

JOURNAL 1 (bases 1 to 1235)

COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LLM12185 row: f column: 23

High quality sequence stop: 495.

Location/Qualifiers

1. .1235

/organism="Homo sapiens"

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/clone="IMAGE:5520790"

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/clone\_1lb="NIH\_MGC\_71"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb.

ORIGIN

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Best Local Similarity 91.3%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACATTTTCAGCGCATAGCGA 24

DB 529 TGACATTTTCAGCGCATAGCGA 507  
|||||

Search completed: February 9, 2005, 21:55:42  
Job time : 2450.85 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-14

Perfect score: 25

Sequence: 1 cgaaccaggcagcgtcgaatggcgga 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pac: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_seq: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504311 Sequence
2	25	100.0	25	6	AX504328 Sequence
3	25	100.0	215	9	HUMMDR1A12
4	25	100.0	2726	6	I33621
5	25	100.0	3840	6	AX481416
6	25	100.0	3843	6	BD171402
7	25	100.0	3852	9	AF537133
8	25	100.0	3852	9	AF537134
9	25	100.0	3852	9	AF582534
10	25	100.0	3860	6	AX323787
11	25	100.0	3860	6	AX323789
12	25	100.0	3924	6	BD190395
13	25	100.0	3924	6	BD234199
14	25	100.0	3924	6	AR380623
15	25	100.0	3924	6	AR452557
16	25	100.0	3924	6	AX024455
17	25	100.0	3924	9	AX409652
18	25	100.0	3924	9	HUMMDR3
19	25	100.0	3988	6	BD190394

c	20	25	100.0	3988	6	AR452556	AR452556 Sequence
c	21	25	100.0	3988	6	AX024454	AX024454 Sequence
c	22	25	100.0	4186	6	AR399194	AR399194 Sequence
c	23	25	100.0	4186	6	AX108654	AX108654 Sequence
c	24	25	100.0	4192	6	AF016535	AF016535 Homo sapi
c	25	25	100.0	4195	6	AR399195	AR399195 Sequence
c	26	25	100.0	4195	6	AX108656	AX108656 Sequence
c	27	25	100.0	4264	6	AR051647	AR051647 Sequence
c	28	25	100.0	4264	6	AR051650	AR051650 Sequence
c	29	25	100.0	4378	6	BD2326	BD2326 Multidrug r
c	30	25	100.0	4553	6	CO716151	CO716151 Sequence
c	31	25	100.0	4643	6	CQ815440	CQ815440 Sequence
c	32	25	100.0	4643	6	AX522070	AX522070 Sequence
c	33	25	100.0	4643	6	AX587788	AX587788 Sequence
c	34	25	100.0	4646	6	BD234195	BD234195 ATP-Bind
c	35	25	100.0	4646	6	CO861565	CO861565 Sequence
c	36	25	100.0	4646	6	I49610	I49610 Sequence 2
c	37	25	100.0	4646	6	AR380622	AR380622 Sequence
c	38	25	100.0	4646	6	AX336420	AX336420 Sequence
c	39	25	100.0	4646	6	AX336708	AX336708 Sequence
c	40	25	100.0	4646	6	AX391099	AX391099 Sequence
c	41	25	100.0	4646	6	AX504298	AX504298 Sequence
c	42	25	100.0	4646	9	HUMMDR1	M14758 Homo sapien
c	43	25	100.0	4669	6	AR055785	AR055785 Sequence
c	44	25	100.0	4669	6	AR091275	AR091275 Sequence
c	45	25	100.0	4669	6	I08557	I08557 Sequence 3

#### ALIGNMENTS

RESULT 1	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
DEFINITION	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
ACCESSION	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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AUTHORS	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
TITLE	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
JOURNAL	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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Mismatches	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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DB	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Conservative	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Mismatches	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Indels	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Gaps	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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Mismatches	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Indels	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Gaps	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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Gaps	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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Gaps	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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Mismatches	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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Gaps	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
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DB	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Conservative	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
Mismatches	AX504311	Sequence 14 from Patent				

REFERENCE 1  
AUTHORS Colgan, S.P.  
TITLE Compositions and methods for treating hematologic malignancies and multiple drug resistance  
JOURNAL Patent: WO 0234291-A 31 02-MAY-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"

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Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25  
Db 25 CGAACGAGGCGACGTGCATGGCGA 1

RESULT 3  
LOCUS HUMMDR1A12/c 215 bp DNA linear PRI 08-JAN-1995  
DEFINITION Human P-glycoprotein (MDR1) gene, exon 14.  
ACCESSION M29433.1 J05168  
VERSION M29433.1 GI:187482  
KEYWORDS P-glycoprotein; multidrug resistance.  
SEGMENT 12 of 26  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 215)  
AUTHORS Chen, C.J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and  
Ronsinson, I.B.  
TITLE Genomic organization of the human multidrug resistance (MDR1) gene  
and origin of P-glycoproteins  
JOURNAL J. Biol. Chem. 265 (1), 506-514 (1990)  
MEDLINE 90094448  
PUBMED 1967175  
COMMENT Original source text: Human multidrug resistant cell line KB-VL  
DNA.  
Draft entry and computer-readable sequence for [1] kindly submitted  
by I.B.Ronsinson, 27-OCT-1989.  
FEATURES Location/Qualifiers  
source 1..215  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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189..215  
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ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25  
Db 103 CGAACGAGGCGACGTGCATGGCGA 79

RESULT 4  
LOCUS I33621 2726 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5593840.  
ACCESSION I33621  
VERSION I33621.1 GI:1824412  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2726)  
AUTHORS Bhattachar, S.K., George, A.L. Jr. and Nazarenko, I.  
TITLE Amplification of nucleic acid sequences  
JOURNAL Patent: US 5593840-A 1 14-JAN-1997;  
FEATURES Location/Qualifiers  
source 1..2726  
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ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 2726;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25  
Db 144 CGAACGAGGCGACGTGCATGGCGA 120

RESULT 5  
LOCUS AX481416 3840 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 30 from Patent WO02055693.  
ACCESSION AX481416  
VERSION AX481416.1 GI:22316330  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 02055693-A 30 18-JUL-2002;  
Ribopharma AG (DE)  
FEATURES Location/Qualifiers  
source 1..3840  
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Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25  
Db 1637 CGAACGAGGCGACGTGCATGGCGA 1613

RESULT 6  
LOCUS BD171402 3843 bp DNA linear PAT 18-FEB-2003  
DEFINITION Method for predicting side effects of immunosuppressant and primer  
used therefor.  
ACCESSION BD171402  
VERSION BD171402.1 GI:28412692

KEYWORDS JP 2002223769-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3843)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
TITLE  
JOURNAL  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002223769-A/1  
PD 13-AUG-2002  
PF 31-JAN-2001 JP 2001024723  
PI ICHIRO IEIRI  
PC C12N15/09, C1201/68, C12N15/00  
CC Method for predicting side effects of immunosuppressant and  
CC primer used  
CC therefor  
FH Key  
FT source  
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Query Match 100.0%; Score 25; DB 6; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGAACCGGCGACGTGCATGGCGA 25  
DB 1640 CGAACCGGCGACGTGCATGGCGA 1616  
RESULT 7  
AF537133/c 3852 bp mRNA linear PRI 11-SEP-2002  
LOCUS Macaca mulatta multidrug resistance p-glycoprotein mRNA, complete  
DEFINITION  
cde.  
ACCESSION AF537133  
VERSION AF537133.1 GI:22775295  
KEYWORDS  
SOURCE  
ORGANISM  
Macaca mulatta (rhesus monkey)  
Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
REFERENCE 1 (bases 1 to 3852)  
AUTHORS Hanekom, S.R., Xiao, G. and Crespi, C.L.  
TITLE Rhesus monkey P-glycoprotein mRNA  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3852)  
AUTHORS Hanekom, S.R., Xiao, G. and Crespi, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (09-AUG-2002) BD Biosciences, 6 Henshaw Street, Woburn,  
MA 01801, USA  
FEATURES  
source Location/Qualifiers  
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Query Match 100.0%; Score 25; DB 9; Length 3852;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGAACCGGCGACGTGCATGGCGA 25  
DB 1649 CGAACCGGCGACGTGCATGGCGA 1625  
RESULT 8  
AF537134/c 3852 bp mRNA linear PRI 06-JUN-2003  
LOCUS Macaca fascicularis multidrug resistance p-glycoprotein mRNA,  
DEFINITION  
complete cds.  
ACCESSION AF537134  
VERSION AF537134.2 GI:31442762  
KEYWORDS  
SOURCE  
ORGANISM  
Macaca fascicularis (crah-eating macaque)  
Macaca fascicularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
REFERENCE 1 (bases 1 to 3852)  
AUTHORS Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.  
TITLE Cynomolgous monkey P-glycoprotein mRNA  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3852)  
AUTHORS Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (09-AUG-2002) BD Biosciences, 6 Henshaw Street, Woburn,  
MA 01801, USA  
REFERENCE 3 (bases 1 to 3852)  
AUTHORS Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2003) BD Biosciences, 6 Henshaw Street, Woburn,  
MA 01801, USA  
REMARK  
COMMENT Sequence update by submitter  
ON Jun 6, 2003 this sequence version replaced gi:22775297.  
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## ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 3852;  
Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCAATGGCGA 25  
Db 1649 CGAACGAGGCGACGTGCAATGGCGA 1625

RESULT 9  
AY582534/c 3852 bp mRNA linear PRI 20-APR-2004  
LOCUS Macaca mulatta multidrug resistance protein (MDR1) mRNA, complete  
DEFINITION cds.

ACCESSION AY582534  
VERSION AY582534.1 GI:46394983  
KEYWORDS  
SOURCE  
ORGANISM Macaca mulatta (rhesus monkey)  
Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Macaca.

REFERENCE  
AUTHORS 1 (bases 1 to 3852)  
TITLE Booth-Genthe, C.L., Roller, C.R. and Rushmore, T.H.  
JOURNAL Cloning of Macaca mulatta MDR1  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 3852)  
TITLE Booth-Genthe, C.L., Roller, C.R. and Rushmore, T.H.  
JOURNAL Direct Submission  
TITLE Submitted (25-MAR-2004) Drug Metabolism, Merck Research  
JOURNAL Laboratories, WP75A-203, West Point, PA 19486, USA

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gene  
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OEKFEHMTDOSLOVPYRNSLRKAIHFIITSTFOAMVFSYAGCFRGAVALVASHLM  
SPEDLVFSAVFGAMAVGVSPAPYAKASAAHIMIIEKTPIDISYSTEGLK  
PNTLEGNVFNENVPYTRLDIPVLOGLSEVKKQTLALVSGSGCKSTVOLLER  
FADPLAGKVLIDGKEIKQNVOMLRALHIGVSOEPIIFDCISENIAVGNDSRVSOE  
BIVRAKXENIHAFTESLPNKYSTRVGDKGTOLSGGCKORIAIARLVROPHILLDE  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCAATGGCGA 25  
Db 1649 CGAACGAGGCGACGTGCAATGGCGA 1625

RESULT 10  
AX322787/c 3860 bp DNA linear PAT 07-JAN-2002  
LOCUS Sequence 1 from Patent WO0192877.  
DEFINITION AX322787  
ACCESSION AX322787  
VERSION AX322787.1 GI:18093766  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Sorrentino, B. and Schuetz, J.  
JOURNAL Method of identifying and/or isolating stem cells  
PATENT: WO 0192877-A 1 06-DEC-2001;  
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCAATGGCGA 25  
Db 1640 CGAACGAGGCGACGTGCAATGGCGA 1616

RESULT 11  
AX322789/c 3860 bp DNA linear PAT 07-JAN-2002  
LOCUS Sequence 3 from Patent WO0192877.  
DEFINITION AX322789  
ACCESSION AX322789  
VERSION AX322789.1 GI:18093767  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Sorrentino, B. and Schuetz, J.  
TITLE Method of identifying and/or isolating stem cells  
JOURNAL Patent: WO 0192877-A 3 06-DEC-2001;  
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)  
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Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1640 CGAACCAGGCGACGTGCATGGCGA 1616  
RESULT 12  
BD190395/c 3924 bp DNA linear PAT 17-JUL-2003  
LOCUS Phosphatidylcholine as a medicament for the protection of mucosa.  
DEFINITION BD190395  
ACCESSION BD190395.1 GI:33000134  
VERSION JP 2002522381-A/2.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3924)  
AUTHORS Stremmel, W.  
TITLE Phosphatidylcholine as a medicament for the protection of mucosa  
JOURNAL Patent: JP 2002522381-A 2 23-JUL-2002;  
Wolfgang Stremmel  
COMMENT OS Homo sapiens  
PN JP 2002522381-A/2  
PD 23-JUL-2002  
PF 06-AUG-1999 JP 2000563262  
PR 06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DE 198 57 750.8 PI  
Wolfgang Stremmel  
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Db 1678 CGAACCAGGCGACGTGCATGGCGA 1654  
RESULT 13  
BD234199/c 3924 bp DNA linear PAT 17-JUL-2003  
LOCUS ATP-binding cassette genes and proteins for diagnosis and remedy of  
DEFINITION BD234199  
ACCESSION BD234199.1 GI:33043969  
VERSION JP 2002525111-A/9.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 3924)  
TITLE ATP-binding cassette genes and proteins for diagnosis and remedy of  
JOURNAL lipid disorders and inflammatory diseases  
Patent: JP 2002525111-A 9 13-AUG-2002;  
BAYER AKTIENGESELLSCHAFT  
COMMENT OS Homo sapiens (human)  
PN JP 2002525111-A/9  
PD 13-AUG-2002  
PF 21-SEP-1999 JP 2000572359  
PR 25-SEP-1998 US 60/101706  
PI GERD SCHMITZ, JOCHEN KLUCKEN  
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P3/06,A61P9/10, PC  
A61P29/00,  
PC C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC  
,C12P21/02,C12Q1/68,  
PC G01N33/53,C12N15/00,C12N5/00,A61K37/02  
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FH Key location/Qualifiers  
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Db 1678 CGAACCAGGCGACGTGCATGGCGA 1654  
RESULT 14  
AR380623/c 3924 bp DNA linear PAT 18-DEC-2003  
LOCUS Sequence 1168 from patent US 6607879.  
DEFINITION AR380623  
ACCESSION AR380623  
VERSION AR380623.1 GI:40088257  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3924)  
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.  
TITLE Compositions for the detection of blood cell and immunological  
JOURNAL response gene expression  
Patent: US 6607879-A 1168 19-AUG-2003;  
FEATURES location/Qualifiers  
source 1..3924  
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Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGAACCAGGCGACGTGCATGGCGA 25  
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Db 1678 CGAACCAGGCGACGTGCATGGCGA 1654  
RESULT 15  
AR452557/c 3924 bp DNA linear PAT 20-FEB-2004  
LOCUS Sequence 2 from patent US 6677319.  
DEFINITION AR452557  
ACCESSION AR452557

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VERSION      AR452557.1  GI:42684345
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 3924)
AUTHORS      Stremmel, W.
TITLE        Phosphatidylcholine as medication with protective effect large
JOURNAL      intestinal mucosa
FEATURES     Patent: US 6677319-A 2.13.-JAN-2004;
              location/Qualifiers
              1..3924
              /organism="unknown"
              /mol_type="genomic DNA"

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Query Match      100.0%; Score 25; DB 6; Length 3924;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGAACGAGGCGACCTGCAATGGCGA 25
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Db      1678 CGAACGAGGCGACCTGCAATGGCGA 1654

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OM nucleic - nucleic search, using 6w model

Run on: February 9, 2005, 13:42:01 ; Search time 78.592 Seconds  
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#### SUMMARIES

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C 1	25	100.0	2726	1 US-08-461-823-1	Sequence 1, Appl1
C 2	25	100.0	3924	4 US-09-023-655-1168	Sequence 1168, Ap
C 3	25	100.0	3924	4 US-09-762-195-2	Sequence 2, Appl1
C 4	25	100.0	3988	4 US-09-762-195-1	Sequence 1, Appl1
C 5	25	100.0	4186	4 US-09-672-810-1	Sequence 1, Appl1
C 6	25	100.0	4195	4 US-09-672-810-3	Sequence 3, Appl1
C 7	25	100.0	4264	2 US-08-784-6498-1	Sequence 1, Appl1
C 8	25	100.0	4264	2 US-08-784-6498-5	Sequence 5, Appl1
C 9	25	100.0	4646	1 US-08-181-471-2	Sequence 2, Appl1
C 10	25	100.0	4646	4 US-09-023-655-1167	Sequence 1167, Ap
C 11	25	100.0	4669	2 US-08-583-276-18	Sequence 18, Appl
C 12	25	100.0	4669	2 US-08-752-447-1	Sequence 1, Appl1
C 13	25	100.0	4669	3 US-09-316-167-1	Sequence 1, Appl1
C 14	25	100.0	4669	4 US-09-397-233-1	Sequence 1, Appl1
C 15	25	100.0	4669	6 5206352-3	Sequence 1, Appl1
C 16	25	100.0	4669	6 5206352-3	Patent No. 5206352
C 17	25	100.0	4669	6 5206352-3	Patent No. 5206352
C 18	25	100.0	8630	4 US-08-793-610-5	Sequence 5, Appl1
C 19	25	100.0	8630	4 US-09-306-417-1	Sequence 1, Appl1
C 20	25	100.0	9318	2 US-09-306-417-2	Sequence 2, Appl1
C 21	25	100.0	9318	2 US-08-793-610-6	Sequence 6, Appl1
C 22	21.8	87.2	4279	4 US-09-672-725C-1	Sequence 1, Appl1
C 23	21.8	87.2	4279	4 US-09-672-725C-22	Sequence 22, Appl1
C 24	21.8	87.2	4279	4 US-09-672-725C-24	Sequence 24, Appl1
C 25	21.8	87.2	4317	4 US-09-672-725C-3	Sequence 3, Appl1
C 26	21.8	87.2	4317	4 US-10-044-671-1	Sequence 1, Appl1
C 27	20.2	80.8	4233	3 US-09-120-513-1	Sequence 1, Appl1

C 28	20.2	80.8	4233	3 US-09-450-105-1	Sequence 1, Appl1
C 29	18.6	74.4	4047	2 US-08-612-734B-1	Sequence 1, Appl1
C 30	18.6	74.4	4800	2 US-08-612-734B-3	Sequence 3, Appl1
C 31	18.2	72.8	601	4 US-09-540-236-1532	Sequence 1532, Ap
C 32	17.8	71.2	601	4 US-09-949-016-191243	Sequence 191243,
C 33	17.8	71.2	601	4 US-09-949-016-191244	Sequence 191244,
C 34	17.8	71.2	30847	4 US-09-949-016-16657	Sequence 16657, A
C 35	17.8	71.2	121970	4 US-09-949-016-17216	Sequence 17216, A
C 36	17.6	70.4	654	4 US-09-252-991A-9404	Sequence 9404, Ap
C 37	17.6	70.4	771	4 US-09-252-991A-9372	Sequence 9372, Ap
C 38	17.6	70.4	813	4 US-09-252-991A-9462	Sequence 9462, Ap
C 39	17.6	70.4	1110	4 US-09-328-352-7779	Sequence 2779, Ap
C 40	17.6	70.4	1341	4 US-09-902-540-7697	Sequence 7697, Ap
C 41	17.6	70.4	6404	4 US-09-902-540-760	Sequence 760, App
C 42	17.2	68.8	702	4 US-09-583-110-92	Sequence 92, Appl
C 43	17.2	68.8	708	4 US-09-107-433-1098	Sequence 1098, Ap
C 44	17.2	68.8	10690	3 US-08-961-527-93	Sequence 93, Appl
C 45	17.2	68.8	17907	4 US-09-949-016-13189	Sequence 13189, A

#### ALIGNMENTS

RESULT 1  
US-08-461-823-1/c  
Sequence 1, Application US/08461823  
Patent No. 5593840  
GENERAL INFORMATION:  
APPLICANT: Bhatnagar, Satish K.  
APPLICANT: George Jr., Albert L.  
APPLICANT: Nazarenko, Irina  
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACID SEQUENCES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESS: OncoPharm, Inc.  
STREET: 200 Perry Parkway  
CITY: Gaithersburg  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20877  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08461,823  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/168,621  
FILING DATE: 16-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/010,433  
FILING DATE: 27-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Karta, Glenn E.  
REGISTRATION NUMBER: 30,649  
REFERENCE/DOCKET NUMBER: PA-0012 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301 527-2058  
TELEFAX: 301 208-6997  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2726 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-461-823-1

Query Match 100.0%; Score 25; DB 1; Length 2726;  
Best Local Similarity 100.0%; Pred. No. 0.087;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 144 CGAACGAGGCGACGTGCATGGCGA 120

## RESULT 2

US-09-023-655-1168/c  
Sequence 1168, Application US/09023655  
Patent No. 6607879

GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
FILING DATE: HEREWITH  
APPLICATION NUMBER: US/09/023,655

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELEPHONE: (650) 955-0555  
TELEFAX: (650) 945-4166

## INFORMATION FOR SEQ ID NO: 1168:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3924 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

## IMMEDIATE SOURCE:

LIBRARY: GENBANK  
CLONE: g187501

US-09-023-655-1168

Query Match 100.0%; Score 25; DB 4; Length 3924;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCATGGCGA 25  
DB 1678 CGAACGAGGCGACGTGCATGGCGA 1654

## RESULT 3

US-09-762-195-2/c  
Sequence 2, Application US/09762195  
Patent No. 6677319  
GENERAL INFORMATION:  
APPLICANT: Stremmel, Wolfgang

TITLE OF INVENTION: Phosphatidylcholine as Medication with  
TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa  
FILE REFERENCE: 34691/208520  
CURRENT APPLICATION NUMBER: US/09/762,195  
CURRENT FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: PCT/EP99702426  
PRIOR FILING DATE: 1999-08-06  
PRIOR APPLICATION NUMBER: 198 35 526 2 DE  
PRIOR FILING DATE: 1998-08-06  
PRIOR APPLICATION NUMBER: 198 57 570.8 DE  
PRIOR FILING DATE: 1998-12-15  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 3924  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-762-195-2

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Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCATGGCGA 25  
DB 1678 CGAACGAGGCGACGTGCATGGCGA 1654

## RESULT 4

US-09-762-195-1/c  
Sequence 1, Application US/09762195  
Patent No. 6677319

## GENERAL INFORMATION:

APPLICANT: Stremmel, Wolfgang  
TITLE OF INVENTION: Phosphatidylcholine as Medication with  
TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa  
FILE REFERENCE: 34691/208520  
CURRENT APPLICATION NUMBER: US/09/762,195  
CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: PCT/EP99702426  
PRIOR FILING DATE: 1999-08-06

PRIOR APPLICATION NUMBER: 198 35 526 2 DE  
PRIOR FILING DATE: 1998-08-06

PRIOR APPLICATION NUMBER: 198 57 570.8 DE  
PRIOR FILING DATE: 1998-12-15

NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3988

TYPE: DNA

ORGANISM: Homo sapiens

US-09-762-195-1

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Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCATGGCGA 25  
DB 1706 CGAACGAGGCGACGTGCATGGCGA 1682

## RESULT 5

US-09-672-810-1/c  
Sequence 1, Application US/09672810  
Patent No. 6617450

## GENERAL INFORMATION:

APPLICANT: STOCKER, PENNY J.

APPLICANT: STEIMEL-CRESPI, DOROTHY T.

APPLICANT: CRESPI, CHARLES L.

TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF

FILE REFERENCE: G0307/7018

CURRENT APPLICATION NUMBER: US/09/672,810

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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 4186
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3940)
US-09-672-810-1

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Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
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Db 1739 CGAACGAGGCGACGTGCATGGCGA 1715

RESULT 6
US-09-672-810-3/c
Sequence 3, Application US/09672810
Patent No. 6617450
GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 4195
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3949)
US-09-672-810-3

Query Match          100.0%; Score 25; DB 4; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
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Db 1748 CGAACGAGGCGACGTGCATGGCGA 1724

RESULT 7
US-08-784-649A-1/c
Sequence 1, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: SIKIC, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
```

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STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 5:

US-08-784-649A-1

Query Match          100.0%; Score 25; DB 2; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
    |||||
Db 1778 CGAACGAGGCGACGTGCATGGCGA 1754

RESULT 8
US-08-784-649A-5/c
Sequence 5, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: SIKIC, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 5:
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 4264 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.09;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25  
DB 1778 CGAACGAGGCGACGTGCATGGCGA 1754

RESULT 9  
US-08-181-471-2/c  
Sequence 2, Application US/08181471  
Patent No. 5641508

GENERAL INFORMATION:  
APPLICANT: Li, Lingna  
APPLICANT: Lishko, Valeryi K.  
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL  
TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Thomas Fitting  
STREET: 12526 High Bluff Drive, Suite 300  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92130

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,471  
FILING DATE: 13-JAN-1994  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/041,553  
FILING DATE: 02-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: ANT0029P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-792-3680  
TELEFAX: 619-792-8477

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 4646 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4267  
US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.09;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25  
|||||

DB 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 10  
US-09-023-655-1167/c  
Sequence 1167, Application US/09023655  
Patent No. 6607879

GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Sellhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1167:  
SEQUENCE CHARACTERISTICS:

LENGTH: 4646 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: G187468  
US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.09;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25  
DB 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 11  
US-08-583-276-18/c

Sequence 18, Application US/08583276  
Patent No. 5837536

GENERAL INFORMATION:  
APPLICANT: McDonagh, Kevin T.  
APPLICANT: Nienhuis, Arthur  
APPLICANT: Tolstoshev, Paul  
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES  
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gillilan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DM4 V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,276  
FILING DATE: 05-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/332,444  
FILING DATE: 31-OCT-1994  
APPLICATION NUMBER: 07/887,712  
FILING DATE: 22-MAY-1992  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 bases  
TYPE: nucleic acid  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: Genomic DNA  
US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.09;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACCGAGCGACGTGCATGCGCA 25  
|||||  
Db 2064 CGAACCGAGCGACGTGCATGCGCA 2040

RESULT 12  
US-08-752-447-1/c  
Sequence 1, Application US/08752447  
Patent No. 5994088  
GENERAL INFORMATION:  
APPLICANT: Mechtner, Eugene  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boenken Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,447  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5994088nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001

TELEFAX: 312-913-9808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.09;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACCGAGCGACGTGCATGCGCA 25  
|||||  
Db 2064 CGAACCGAGCGACGTGCATGCGCA 2040

RESULT 13  
US-09-316-167-1/c  
Sequence 1, Application US/09316167  
Patent No. 6365357  
GENERAL INFORMATION:  
APPLICANT: Mechtner, Eugene  
TITLE OF INVENTION: Methods and Reagents for Preparing and  
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boenken Hulbert & Berghoff Ltd.  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/316,167  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752,447  
FILING DATE: 15-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6365357nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-9808  
TELEFAX: 312-913-0001  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: 5'UTR

LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25  
Db 2064 CGAACGAGGCGACGTGCATGCGCA 2040

RESULT 14  
US-09-397-233-1/c  
Sequence 1, Application US/09397233  
Patent No. 6630327  
GENERAL INFORMATION:  
APPLICANT: Mechtner, Eugene  
Ronsinon, Igor B  
TITLE OF INVENTION: Method and Reagents for Preparing and  
Using Immunological Agents Specific for P-glycoprotein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/397,233  
FILING DATE: 16-Sep-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6630327nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 95,1121-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-397-233-1

Query Match 100.0%; Score 25; DB 4; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25  
Db 2064 CGAACGAGGCGACGTGCATGCGCA 2040

RESULT 15  
5206352-3/c  
Patent No. 5206352  
APPLICANT: Ronsinon, Igor B.; Paetan Ira H.; Gottesman,  
Michael M.  
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/622,836  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 892,575  
FILING DATE: 01-AUG-1986  
APPLICATION NUMBER: 845,610  
FILING DATE: 28-MAR-1986  
SEQ ID NO: 3  
LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25  
Db 2064 CGAACGAGGCGACGTGCATGCGCA 2040

Search completed: February 9, 2005, 17:11:19  
Job time : 79.592 secs

GenCore version 5.1.6  
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OW nucleic - nucleic search, using SW model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds  
(without alignments)  
602.360 Million cell updates/sec

Title: US-10-007-255-14

Perfect score: 25  
Sequence: 1 cgaccaggcgacgtgcaatgacga 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*  
1: geneeqn19808:\*  
2: geneeqn19908:\*  
3: geneeqn20008:\*  
4: geneeqn20018:\*  
5: geneeqn20018:\*  
6: geneeqn20028:\*  
7: geneeqn20028:\*  
8: geneeqn20038:\*  
9: geneeqn20038:\*  
10: geneeqn20038:\*  
11: geneeqn20038:\*  
12: geneeqn20048:\*  
13: geneeqn20048:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	25	6 AAD39013	Aad39013 Human mdr
C 2	25	100.0	25	6 AAD39003	Aad39003 Human mdr
C 3	25	100.0	2307	6 ABS65230	abs65230 cDNA enco
C 4	25	100.0	2726	6 AAO70907	Aag70907 Multidrug
C 5	25	100.0	2726	2 AAO70916	Aag70916 Multidrug
C 6	25	100.0	2726	2 AAT43322	Aat43322 Multidrug
C 7	25	100.0	3837	12 ADH22602	Adh22602 cDNA enco
C 8	25	100.0	3840	6 ABV78146	Abv78146 Human mdr
C 9	25	100.0	3840	6 ABZ35722	Abz35722 Human mdr
C 10	25	100.0	3840	6 ABX09965	Abx09965 Human mdr
C 11	25	100.0	3840	6 ABQ78185	Abq78185 Human MDR
C 12	25	100.0	3852	8 ABT14496	Abt14496 Rhesus mo
C 13	25	100.0	3858	12 ADH22599	Adh22599 cDNA enco
C 14	25	100.0	3860	3 AAZ49332	Aaz49332 Human w11
C 15	25	100.0	3860	3 AAZ49333	Aaz49333 Human G18
C 16	25	100.0	3860	6 ABA94365	Aba94365 Human BCR
C 17	25	100.0	3860	6 ABA94366	Aba94366 Human BCR
C 18	25	100.0	3924	3 AAZ94742	Aaz94742 Human ATP
C 19	25	100.0	3924	3 AAZ88974	Aaz88974 Human MDR
C 20	25	100.0	3924	3 AAZ88974	Aaz88974 Human MDR

C 21	25	100.0	3924	6 AEN95801	Abn95801 Gene #229
C 22	25	100.0	3924	11 ADI31842	Adi31842 Human CDN
C 23	25	100.0	3988	3 AAZ88973	Aaz88973 Human MDR
C 24	25	100.0	4039	13 ACN43502	Acn43502 Human dia
C 25	25	100.0	4043	13 ACN41836	Acn41836 Human dia
C 26	25	100.0	4148	13 ACN41835	Acn41835 Human dia
C 27	25	100.0	4186	4 AAF86127	Aaf86127 Cynomolog
C 28	25	100.0	4195	4 AAF86128	Aaf86128 Cynomolog
C 29	25	100.0	4264	2 AAV65333	Aav65333 Mutated h
C 30	25	100.0	4264	2 AAV65334	Aav65334 Mutated h
C 31	25	100.0	4349	4 AAH57442	Aah57442 Human int
C 32	25	100.0	4378	2 AAQ04522	Aaq04522 Multidrug
C 33	25	100.0	4533	6 ABS65229	Abs65229 cDNA enco
C 34	25	100.0	4643	6 ABS76368	Ab76368 cDNA enco
C 35	25	100.0	4643	6 ABV94267	Abv94267 Breast ca
C 36	25	100.0	4643	6 ABV74349	Abv74349 Human ABC
C 37	25	100.0	4643	10 ABX77217	Abx77217 cDNA enco
C 38	25	100.0	4643	12 ADP18689	Adp18689 Human MDR
C 39	25	100.0	4643	12 ADP19748	Adp19748 Human PRO
C 40	25	100.0	4643	13 ADP54881	Adp54881 Human PRO
C 41	25	100.0	4646	2 AAO72872	Aao72872 Human mul
C 42	25	100.0	4646	3 AAQ94738	Aaq94738 Human ATP
C 43	25	100.0	4646	6 ABL68592	Ab168592 Kidney ca
C 44	25	100.0	4646	6 ABL68880	Ab168880 Kidney ca
C 45	25	100.0	4646	6 AAD38994	Aad38994 Human mdr

## ALIGNMENTS

RESULT 1  
AAD39013/c  
ID AAD39013 standard; DNA; 25 BP.

AAD39013;  
23-SEP-2002 (first entry)

Human mdr1 gene HIF-1 binding site DNA #6.

Human; haematologic malignancy; multidrug resistance; MDR; SMO-1;  
hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;  
lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
myeloid disorder; lymphocytic leukaemia; thrombocythaemia;  
angioleukemic myeloid metaplasia; myeloid leukaemia; gene therapy;  
polycythaemia vera; hypoxia responsive element; HRE; ds.

Homo sapiens.

Key Location/Qualifiers  
FT misc\_binding 11..15  
FT FT /\*tag= a  
FT FT /bound\_molecule= "HIF-1"

WO200234291-A2.

02-MAY-2002.

25-OCT-2001; 2001WO-US049856.

26-OCT-2000; 2000US-0243542P.

(BGHM ) BRIGHAM & WOMENS HOSPITAL INC.

Colgan SP;

WPI; 2002-471427/50.

Treating a subject (at risk of) having a hematologic malignancy or  
multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia  
inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
binding molecules.

PS Example 2; Page 12; 92pp; English.

XX  
CC The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiosenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is human mdrl  
CC gene HIF-1 binding site DNA

SO Sequence 25 BP; 2 A; 9 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACCGGCGACGTGCATGCGCA 25  
Db 25 CGAACCGGCGACGTGCATGCGCA 1

RESULT 2  
AAD39003 standard; DNA; 25 BP.

XX AAD39003;  
XX  
XX 23-SEP-2002 (first entry)  
XX  
XX  
DE Human mdrl-HRE antisense oligonucleotide #6.  
XX  
XX Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;  
XX hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;  
XX lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
XX myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;  
XX angiosenic myeloid metaplasia; myeloid leukaemia; gene therapy;  
XX polycythaemia vera; hypoxia responsive element; HRE; antisense;  
XX phosphorothioate backbone; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..25  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
XX W0200234291-A2.  
XX  
XX  
XX 02-MAY-2002.  
XX  
XX 25-OCT-2001; 2001WO-US049856.  
XX  
XX 26-OCT-2000; 2000US-0243542P.  
XX  
XX (BGM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX  
XX Colgan SP;  
XX  
XX WPI; 2002-471427/50.  
XX  
XX Treating a subject (at risk of) having a haematologic malignancy or  
XX multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia  
XX inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT binding molecules.

XX  
XX Claim 14; Page 43; 92pp; English.

XX  
CC The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angiosenic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is an antisense  
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its  
CC expression. This oligo is used in the exemplification of the invention

SO Sequence 25 BP; 7 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACCGGCGACGTGCATGCGCA 25  
Db 1 CGAACCGGCGACGTGCATGCGCA 25

RESULT 3  
ABS65230/C  
ID ABS65230 standard; cDNA; 2307 BP.

XX ABS65230;  
XX  
XX 15-NOV-2002 (first entry)  
XX  
XX  
DE cDNA encoding tumour involved gene (TIG) splice variant, NV-31.  
XX  
XX Human; ss; gene; splice variant; tumour-involved gene; TIG;  
XX pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;  
XX endothelial cell; cell differentiation; cell proliferation; apoptosis;  
XX gene therapy.  
XX  
XX Homo sapiens.  
OS  
OS  
XX  
XX US2002086384-A1.  
XX  
XX 04-JUL-2002.  
XX  
XX 13-MAR-2001; 2001US-00805020.  
XX  
XX 14-MAR-2000; 2000IL-00135402.  
XX 16-MAY-2000; 2000IL-00136154.  
XX  
XX (LEVI/) LEVINE Z.  
XX (DAVI/) DAVID A.  
XX (ROMA/) ROMANO C.  
XX (BERN/) BERNSTEIN J.  
XX  
XX Levine Z, David A, Romano C, Bernstein J;  
XX  
XX WPI; 2002-635679/68.  
XX P-PSDB; ABG79700.  
XX  
XX Novel nucleic acid sequence, which is an alternative splicing variant of  
XX tumor involved genes, useful for detecting cancer, predisposition to  
XX cancer, for evaluating cancer state and in gene therapy for treating  
XX cancer.



PS Claim 1; Page 60-61; 180pp; English.

XX The invention discloses isolated human nucleic acid alternative splicing  
 CC variants that are all tumour-involved genes (TIGs). The nucleic acids and  
 CC polypeptides are useful for determining the level of a nucleic acid or  
 CC polypeptide in a biological sample, for detecting a variant nucleic acid  
 CC or polypeptide sequence in a biological sample, for determining the level  
 CC of variant nucleic acid or polypeptide sequences in a biological sample  
 CC and for determining the ratio between the level of variant sequence in a  
 CC first biological sample and the level of the original sequence from which  
 CC the variant has been varied by alternative splicing in a second  
 CC biological sample and for raising antibodies. A pharmaceutical  
 CC composition comprising a carrier and the nucleic acid, is useful for  
 CC treating diseases (e.g. cancer) that can be ameliorated or cured by  
 CC increasing or decreasing the level of the encoded protein. The nucleic  
 CC acids are also useful for diagnostic purposes, especially for detecting  
 CC cancer or a predisposition to cancer, for evaluating the state or  
 CC aggressiveness of cancer disease, in basic research, for understanding  
 CC the physiological function of the original TIG, in targeting or  
 CC developing pharmaceuticals, for distinguishing various stages in the life  
 CC cycle of the same type of cells which may be helpful for the development  
 CC of pharmaceuticals for various cancer stages in which cell cycle is non-  
 CC normal, for determining mutations in tumour-involved genes and in gene  
 CC therapy. The polypeptides are useful for identifying compounds capable of  
 CC binding to the variant product and modulating its activity and for  
 CC modulating endothelial differentiation and proliferation, as well as to  
 CC modulate apoptosis either ex vivo or in vivo. The sequences presented in  
 CC AB5652200-AB565235 are the coding sequences for the new variants (NV) 1-  
 CC 36 of the TIGs disclosed

XX Sequence 2307 BP; 662 A; 441 C; 591 G; 612 T; 0 U; 1 Other;

XX Query Match 100.0%; Score 25; DB 6; Length 2307;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCCAGGCGACGTGCATGCGCA 25

DB 2064 CGAACCCAGGCGACGTGCATGCGCA 2040

RESULT 4  
 AAQ70907/c

ID AAQ70907 standard; DNA; 2726 BP.

XX AAQ70907;

AC 25-MAR-2003 (revised)

DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

XX Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX WO9417206-A1

XX 04-AUG-1994.

XX 12-NOV-1993; 93WO-US010883.

XX 27-JAN-1993; 93US-00010433.

XX (ONCO-) ONCOR INC.

XX Bhatnagar SK, George AL;

XX WPI; 1994-264118/32.

PT Enzymatic amplification of target nucleic acid sequences in a mixt. - to  
 PT detect a mutation or allele in the target, e.g. that causes a genetic  
 PT disease.

XX Disclosure; Page 30; 50pp; English.

XX This gene is used as an example of a target DNA in a method for the  
 CC amplification of nucleic acid sequences in a mixture using various DNA  
 CC probes/primers. The method may be used to detect a mutation or allele in  
 CC the target, e.g. that causes a genetic disease; (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 2; Length 2726;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCCAGGCGACGTGCATGCGCA 25

DB 144 CGAACCCAGGCGACGTGCATGCGCA 120

RESULT 5

AAQ70916/c

ID AAQ70916 standard; DNA; 2726 BP.

XX AAQ70916;

AC 25-MAR-2003 (revised)

DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

XX Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX WO9417210-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US000748.

XX 27-JAN-1993; 93US-00010433.

XX 16-DEC-1993; 93US-00168621.

XX (ONCO-) ONCOR INC.

XX Bhatnagar SK, George AL;

XX WPI; 1994-264122/32.

XX Enzymatic amplification of target nucleic acid sequences to form exact or  
 PT modified copies - has increased fidelity and can identify point mutations  
 PT or allele(s).

XX Disclosure; Page 30; 69pp; English.

XX This gene is used as an example of a target DNA in a method for the  
 CC amplification of nucleic acid sequences in a mixture using various DNA  
 CC probes/primers. The method may be used to detect a mutation or allele in  
 CC the target, e.g. that causes a genetic disease; (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 2; Length 2726;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCCAGGCGACGTGCATGCGCA 25

DB 144 CGAACCCAGGCGACGTGCATGCGCA 120

```
RESULT 6
AAT43322/c
ID AAT43322 standard; DNA; 2726 BP.
XX
AC AAT43322;
XX
DT 01-SEP-1997 (first entry)
XX
DE Multidrug resistance gene-1.
XX
KM PCR primer; amplify; polymerase chain reaction; ligase chain reaction;
XX LCR; human; multidrug resistance gene; MDR-1; ds.
XX
OS Synthetic.
XX
PN WO9639537-A1.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-US008841.
XX
PR 05-JUN-1995; 95US-00461823.
XX
PA (ONCO-) ONCOR INC.
XX
PI Bhatnagar SK, George AL, Nazarenko I;
XX
PI WPI; 1997-043158/04.
XX
PT Amplification method avoiding strand displacement by polymerase - used in
PT the detection of mutation(s) and allele(s) associated with genetic
PT disease and cancer.
XX
PS Example 1; Page 50-51; 92pp; English.
XX
XX This sequence represents the multidrug resistance gene (MDR-1) amplified
CC by the primers shown in AAT43320 and AAT43321. This sequence can be used
CC as a target in the method of the invention, for enzymatically amplifying
CC a target nucleic acid (TNA) sequence contained in a nucleic acid or
CC mixture of nucleic acids while avoiding strand displacement by
CC polymerase. The method comprises using three primers, one complementary
CC to a first segment of the TNA, a second complementary to a second segment
CC of the TNA, which is adjacent to the first primer, and a third which is
CC similar to the first segment of the TNA, and is complementary to a
CC portion of the first primer. The first two primers are hybridised to the
CC TNA, and a fused amplification product is created from the TNA using
CC these two primers. The fused product is dissociated, and hybridised to
CC the third primer, which is then extended. The extended modified
CC amplification product is hybridised to the first two primers, and these
CC two primers are ligated. Each of the primers may be labelled using a
CC different label so that the method can be used to detect the presence of
CC a mutation or allele by detecting whether the labelled primer is
CC contained within the fused amplification product or the extended
CC amplification product. The method of the invention combines certain
CC aspects of a ligase chain reaction (LCR) and polymerase chain reaction
CC (PCR), but is improved compared to LCR due to the reduced number of
CC primers needed, and the fact that the entire TNA sequence does not need
CC to be known
XX
SQ Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;
```

```
Query Match 100.0%; Score 25; DB 2; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CGAACCAGGGCAGCTGCATGGCGA 25
Db 144 CGAACCGAGGCGACGTGCATGGCGA 120
```

```
RESULT 7
ADH22602/c
ID ADH22602 standard; cDNA; 3837 BP.
```

```
XX
AC ADH22602;
XX
DT 11-MAR-2004 (first entry)
XX
DE cDNA encoding a human transporter & ion channel (TRICH) protein SeqID100.
XX
KM gene; ss; human; transporters and ion channel; TRICH; cell proliferative;
XX arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;
XX neurological; epilepsy; stroke; developmental; Cushing's syndrome;
XX hypothyroidism; infection; gene therapy; cytotoxic; antiinflammatory;
XX immunosuppressive; antiaesthetic; anticonvulsant; nootropic;
XX neuroprotective.
XX
OS Homo sapiens.
XX
PN WO2003093444-A2.
XX
PD 13-NOV-2003.
XX
PF 02-MAY-2003; 2003WO-US014026.
XX
PR 03-MAY-2002; 2002US-0377435P.
XX
PR 03-MAY-2002; 2002US-0377444P.
XX
PR 05-JUN-2002; 2002US-0386497P.
XX
PR 11-JUN-2002; 2002US-0388180P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;
XX Emmerling BM, Griffin JA, Hafalia AJA, Ison CH, Jackson AA, Jiang X;
XX Jin P, Kable AE, Khare R, Lee SY, Lee S, Mason PM, Margulis JP;
XX Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Chawla NK;
XX Wilson AD;
XX
XX WPI; 2004-022655/02.
XX
DR P-PSDB; ADH22536.
XX
PT New human transporters and ion channels (TRICH), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant TRICH expression e.g. cancer, AIDS, arteriosclerosis, epilepsy,
PT or infections.
XX
PS Claim 12; SEQ ID NO 100; 448bp; English.
XX
XX This invention relates to novel isolated polynucleotides identified as
CC human transporters and ion channels (TRICH), and the encoded polypeptides
CC thereof. Specifically, it describes using these TRICH molecules, as well
CC as agonists, antagonists, antibodies, expression vectors and host cells,
CC in appropriate screening and toxicity assays to assess the effects of
CC exogenous compounds on TRICH expression. The present invention describes
CC TRICH compositions that are useful in the diagnosis, treatment and
CC prevention of various disorders such as cell proliferative (e.g.
CC arteriosclerosis, cancer, autoimmune/inflammatory (e.g. AIDS, asthma),
CC neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's
CC syndrome hypothyroidism) and for infections. Accordingly, these TRICH
CC molecules can be used for gene therapy purposes and exhibit various
CC activities such as cytostatic, antiinflammatory, immunosuppressive,
CC antiaesthetic, anticonvulsant, nootropic and neuroprotective.
CC Furthermore, a microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions and gene expression
CC profiles. This polynucleotide sequence is a human TRICH cDNA of the
CC invention.
XX
SQ Sequence 3837 BP; 1130 A; 772 C; 962 G; 973 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 25; DB 12; Length 3837;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 CGAACCGAGGCGACGTGCATGGCGA 25
Db 1675 CGAACCGAGGCGACGTGCATGGCGA 1651
```

RESULT 8  
ABV78146/c  
ID ABV78146 standard; DNA; 3840 BP.  
XX  
AC ABV78146;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human mdr-1 DNA SEQ ID NO 30.  
XX  
KM RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;  
KM virocid; protozoacide; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200255693-A2.  
PD 18-JUL-2002.  
PF 09-JAN-2002; 2002WO-EP000152.  
PR 09-JAN-2001; 2001DE-01000586.  
PR 26-OCT-2001; 2001DE-01055280.  
PR 29-NOV-2001; 2001DE-01058411.  
PR 07-DEC-2001; 2001DE-01060151.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
PI Kreutzler R, Lämmer S, Roet S, Hadwiger P;  
DR WPI; 2002-590671/63.  
XX  
PT Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
PT target and having an overhang.  
XX  
PS Claim 10; Page 131-132; 203pp; German.  
XX  
CC The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (ast) of dsRNA is complementary to (I) and at least one end of dsRNA  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in plasmodium or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention  
XX  
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCAATGGCGA 25  
DB 1637 CGAACCGGCGACGTGCAATGGCGA 1613

RESULT 9  
ABZ35722/c  
ID ABZ35722 standard; DNA; 3840 BP.  
XX  
AC ABZ35722;  
XX  
DT 07-FEB-2003 (first entry)  
XX  
DE Human mdr-1 polynucleotide SEQ ID NO 30.

XX  
KM Double stranded RNA; dsRNA; RNA inhibition; cytostatic; virocid;  
KM protozoacide; gene expression; antitumor; infection; plasmodium;  
KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
KM Hepatitis C virus; human papilloma virus; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100588-A1.  
PD 18-JUL-2002.  
PF 09-JAN-2001; 2001DE-01000588.  
PR 09-JAN-2001; 2001DE-01000588.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
PI Kreutzler R, Lämmer S, Roet S, Hadwiger P;  
DR WPI; 2002-683450/74.  
XX  
PT Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are complementary  
PT to the target.  
XX  
PS Claim 13; Page 27-28; 100pp; German.  
XX  
CC The invention relates to inhibiting expression of a target gene in a cell  
CC by introducing at least two oligonucleotides (dsRNA and II), both  
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least part of one strand (S1, S2) of the ds structures in each  
CC of dsRNA and II are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumors  
CC or infections, especially by plasmodium or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is improved  
CC and efficiency can be increased further by pretreating the cells with  
CC interferon. The present sequence is that of a target DNA of the invention  
XX  
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCAATGGCGA 25  
DB 1637 CGAACCGGCGACGTGCAATGGCGA 1613

RESULT 10  
ABX09965/c  
ID ABX09965 standard; DNA; 3840 BP.  
XX  
AC ABX09965;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Human mdr-1 DNA fragment SEQ ID 30.  
XX  
KM Oligonucleotide; interferon; oncogene; cytokine; id; developmental;  
KM prion; inhibition; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100587-C1.  
PD 21-NOV-2002.  
XX

PF 09-JAN-2001; 2001DE-01000587.  
XX  
PR 09-JAN-2001; 2001DE-01000587.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzner R, Limmer S, Roest S, Hadwiger P;  
DR WPI; 2002-742209/81.  
XX  
PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by  
PT introduction of complementary double-stranded oligoribonucleotide, after  
PS treating the cell with interferon.  
PS Disclosure; Page 32-33; 98pp; German.  
XX  
CC This invention describes a novel method for inhibiting expression of a  
CC target gene by introducing into the cell that contains the target gene at  
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)  
CC structure of not more than 49 consecutive nucleotides (nt), where at  
CC least a segment of one strand of the ds structure is complementary with  
CC the target gene and the cells are treated with interferon before  
CC introduction of dsRNA. The method is used to inhibit expression of  
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)  
CC protein genes; developmental or prion genes, or genes expressed in  
CC pathogenic organisms (particularly plasmodia) or in viruses or viroids  
CC (pathogenic in humans, animals or plants). Treating the cells with  
CC interferon greatly increases the extent to which dsRNA can inhibit  
CC expression of the target genes, and the effect is even greater when dsRNA  
CC are modified to increase their stability. ABX09936-ABX10075 represent  
CC gene fragments used to illustrate the method of the invention  
SQ  
Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CGAACCGGGCAGCTGCATGCGCA 25  
Db 1637 CGAACCGGGCAGCTGCATGCGCA 1613  
RESULT 11  
ABL91687/C  
ID ABL91687 standard; DNA; 3840 BP.  
XX  
AC ABL91687;  
XX  
DT 28-MAY-2002 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 30.  
XX  
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;  
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;  
KW cytostatic; virucide; protozoicide; antibacterial; ds.  
XX  
OS Homo sapiens.  
XX  
DE10100586-C1.  
XX  
PD 11-APR-2002.  
XX  
PF 09-JAN-2001; 2001DE-01000586.  
XX  
PR 09-JAN-2001; 2001DE-01000586.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzner R, Limmer S, Roest S, Hadwiger P;  
DR WPI; 2002-270454/32.  
XX

PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by  
PT introducing double-stranded complementary oligorRNA having unpaired  
PT terminal bases.  
XX  
XX Claim 13; Page 28-30; 104pp; German.  
XX  
CC The invention relates to a method for inhibiting expression of a target  
CC gene (ABL91658-ABL91797) in a cell by introducing at least one  
CC oligoribonucleotide that has a double-stranded structure consisting of at  
CC most 49 sequential nucleotide pairs, with at least part of one strand  
CC complementary with the target gene and has at least one end a single-  
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for  
CC antisense inhibition of gene expression useful e.g. for treating tumors  
CC but the oligoribonucleotides may also be directed against genes present  
CC in pathogens (e.g. Plasmodium or viruses/viroids; pathogenic on humans,  
CC animals or plants) or against cytokine, Id, developmental or prion genes.  
CC The method provides more effective inhibition of gene expression than use  
CC of known oligonucleotides, probably because the unpaired overhang  
CC increases stability and thus intracellular concentration  
SQ  
Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CGAACCGGGCAGCTGCATGCGCA 25  
Db 1637 CGAACCGGGCAGCTGCATGCGCA 1613  
RESULT 12  
ABQ78185/C  
ID ABQ78185 standard; cDNA; 3843 BP.  
XX  
AC ABQ78185;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human MDR1 encoding cDNA SEQ ID NO 1.  
XX  
KW Human; immunosuppressant; tacrolimus; cyclosporin; MDR1; SNP;  
KW single nucleotide polymorphism; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..3843 /\*tag= a  
FT CDS /product= "MDR1"  
FT variation replace(2677,A/T)  
FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism"  
XX  
PN JP2002223769-A.  
XX  
PD 13-AUG-2002.  
XX  
PF 31-JAN-2001; 2001JP-00024723.  
XX  
PR 31-JAN-2001; 2001JP-00024723.  
XX  
PA (SRLS-) SRL KK.  
XX  
XX WPI; 2002-639348/69.  
DR P-PSDB; ABB83950.  
XX  
PT Presuming the side effect of an immunosuppressant comprises using a  
PT primer set.  
XX  
PS Disclosure; Page 6-11; 14pp; Japanese.  
XX  
CC The invention relates to presumption of the side effect of at least one

CC immunosuppressant selected from tacrolimus and cyclosporin in which if  
CC the 2677th base in the position of MDR1 gene in the encoding region of  
CC the cDNA sequence is guanine, adenine or thymine, is investigated. The  
CC method is used for the presumption of the side effect of an  
CC immunosuppressant. The present sequence is that of the MDR1 encoding cDNA  
CC of the invention.

XX Sequence 3843 BP; 1129 A; 740 C; 956 G; 1018 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 6; Length 3843;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CGAACGAGGCGACGTGCATGCGCA 25

XX 1640 CGAACGAGGCGACGTGCATGCGCA 1616

XX RESULT 13

XX ABR14496/C

XX ABR14496 standard; cDNA; 3852 BP.

XX ABR14496;

XX 03-APR-2003 (first entry)

XX Rheus monkey P-glycoprotein coding sequence.

XX Rheus monkey; gene; ss; P-glycoprotein inhibitor; drug bioavailability;

XX P-glycoprotein; P-glycoprotein transporter-related disease.

XX Macaca mulatta.

XX WO200274048-A2.

XX 26-SEP-2002.

XX 19-MAR-2002; 2002WO-US008325.

XX 19-MAR-2001; 2001US-0277095P.

XX (GENT-) GENTEST CORP.

XX Creep1 CL, Hanacom SR;

XX MPI: 2003-075423/07.

XX P-PSDB; AAO16036.

XX Isolated nucleic acid molecule encoding a P-glycoprotein of rheus

XX monkey, useful in assays for evaluating bioavailability of drugs, as well

XX as for the optimization or discovery of drugs.

XX Claim 3; Page 51-56; 103pp; English.

XX The invention comprises the amino acid and coding sequence of a rheus

XX monkey (Macaca mulatta) P-glycoprotein and related P-glycoproteins. The

XX cDNA and protein sequences of the invention are useful in assays for

XX evaluating the bioavailability of drugs, as well as the optimization or

XX discovery of drugs for the treatment of disease associated with P-

XX glycoprotein transporter activity. The present cDNA sequence encodes the

XX Rheus monkey P-glycoprotein of the invention

XX Sequence 3852 BP; 1123 A; 750 C; 967 G; 1012 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 8; Length 3852;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CGAACGAGGCGACGTGCATGCGCA 25

XX 1649 CGAACGAGGCGACGTGCATGCGCA 1625

XX RESULT 14

XX ADH22599/C

XX ADH22599 standard; cDNA; 3858 BP.

XX ADH22599;

XX 11-MAR-2004 (first entry)

XX cDNA encoding a human transporter & ion channel (TRICH) protein SeqID97.

XX gene; ss; human; transporters and ion channel; TRICH; cell proliferative;

XX arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;

XX neurological; epilepsy; stroke; developmental; Cushing's syndrome;

XX hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;

XX immunosuppressive; antiepileptic; anticonvulsant; neurotropic;

XX neuroprotective.

XX Homo sapiens.

XX WO2003093444-A2.

XX 13-NOV-2003.

XX 02-MAY-2003; 2003WO-US014026.

XX 03-MAY-2002; 2002US-0377435P.

XX 03-MAY-2002; 2002US-0377444P.

XX 05-JUN-2002; 2002US-0386497P.

XX 11-JUN-2002; 2002US-0388180P.

XX (INCY-) INCYTE CORP.

XX Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;

XX Emerling BM, Griffin JA, Hafalia AA, Ison CH, Jackson AA, Jiang X;

XX Jin P, Kable AE, Khate R, Lee SY, Lee S, Mason PM, Margulis JP;

XX Rankumar J, Richardson TW, Swarnakar A, Tian UK, Chawla NK;

XX Wilson AD;

XX MPI: 2004-022655/02.

XX P-PSDB; ADH22533.

XX New human transporters and ion channels (TRICH), useful for diagnosing,

XX treating and preventing diseases or conditions associated with the

XX aberrant TRICH expression e.g. cancer, AIDS, arteriosclerosis, epilepsy,

XX or infections.

XX Claim 12; SEQ ID NO 97; 448pp; English.

XX This invention relates to novel isolated polynucleotides identified as

XX human transporters and ion channels (TRICH), and the encoded polypeptides

XX thereof. Specifically, it describes using these TRICH molecules, as well

XX as agonists, antagonists, antibodies, expression vectors and host cells,

XX in appropriate screening and toxicity assays to assess the effects of

XX exogenous compounds on TRICH expression. The present invention describes

XX TRICH compositions that are useful in the diagnosis, treatment and

XX prevention of various disorders such as cell proliferative (e.g.

XX arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma),

XX neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's

XX syndrome, hypothyroidism) and for infections. Accordingly, these TRICH

XX molecules can be used for gene therapy purposes and exhibit various

XX activities such as cytostatic, antiinflammatory, immunosuppressive,

XX antiepileptic, anticonvulsant, neurotropic and neuroprotective.

XX Furthermore, a microarray is useful in monitoring or measuring protein-

XX protein interactions, drug-target interactions and gene expression

XX profiles. This polynucleotide sequence is a human TRICH cDNA of the

XX invention.

XX Query Match 100.0%; Score 25; DB 12; Length 3858;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CGAACGAGGCGACGTGCATGCGCA 25

XX 1649 CGAACGAGGCGACGTGCATGCGCA 1625

QY 1 CGAACCGAGGCACTGCAATGGCGA 25  
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 CC AA249332/C  
 CC ID AA249332 standard; cDNA; 3660 BP.  
 CC XX  
 CC AC AA249332;  
 CC DT 14-MAR-2000 (first entry)  
 CC XX  
 CC DE Human wild-type multidrug resistance-1 (MDR-1) cDNA.  
 CC XX  
 CC KM Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;  
 CC KM haematopoietic stem cell; transduction; bone marrow transplantation;  
 CC KM chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;  
 CC KM genetic defect; thalassemia; Gaucher's disease; sickle cell anaemia;  
 CC KM leukaemia; ex vivo expansion; cytokine; wild-type; ds.  
 CC XX  
 CC OS Homo sapiens.  
 CC XX  
 CC FH Key Location/Qualifiers  
 CC FT 1..3843  
 CC FT /\*tag= a  
 CC FT /product= "Human wild-type MDR-1 protein"  
 CC FT replace(553..555, GTT)  
 CC FT /\*tag= b  
 CC FT /note= "cDNA sequence of G185V human mutant MDR-1 given  
 CC FT in AA249333"  
 CC XX  
 CC PN WO9961589-A2.  
 CC XX  
 CC PD 02-DEC-1999.  
 CC XX  
 CC PF 27-MAY-1999; 99WO-US011825.  
 CC XX  
 CC PR 28-MAY-1998; 98US-0086988P.  
 CC XX  
 CC PA (SUTD-) ST JUDE CHILDREN'S RES HOSPITAL.  
 CC XX  
 CC PI Sorrentino B, Bunting K;  
 CC XX  
 CC DR MPI; 2000-072615/06.  
 CC DR P-PSDB; AAY58186.  
 CC XX  
 CC FT Ex vivo expansion of hematopoietic stem cells transduced with a sequence  
 CC FT encoding human multidrug resistance-1, used for bone marrow  
 CC FT transplantation.  
 CC XX  
 CC PS Claim 10; Page 68-70; 113pp; English.  
 CC XX  
 CC CC This sequence represents cDNA encoding human wild-type multidrug  
 CC CC resistance protein MDR-1. MDR-1 is a transmembrane efflux pump,  
 CC CC responsible for the export of drugs from cells, particularly cancer  
 CC CC cells. Wild-type MDR-1 shows increased resistance to etoposide and  
 CC CC decreased resistance to vinca alkaloids compared with a mutant form  
 CC CC (AA58187) where the Gly at position 185 is replaced by Val. The  
 CC CC invention relates to transducing haematopoietic stem cells with nucleic  
 CC CC acid encoding an MDR protein and culturing the modified cells. The  
 CC CC modified haematopoietic stem cells are useful in bone marrow  
 CC CC transplantation (to reconstitute haematopoietic systems in patients who  
 CC CC have undergone chemotherapy or radiation therapy) and in ex vivo gene  
 CC CC therapy of genetic defects in cells derived from haematopoietic stem  
 CC CC cells, e.g., thalassemia, Gaucher's disease, sickle cell anaemia or  
 CC CC leukaemia. The modified cells can also be used to identify factors  
 CC CC involved in regulating proliferation and differentiation in  
 CC CC haematopoietic stem cells. Haematopoietic stem cells that express MDR-1  
 CC CC will be protected against chemotherapeutic agents, so can be engrafted  
 CC CC while the patient is undergoing chemotherapy. Expansion of (rare)  
 CC CC haematopoietic stem cells provides sufficient cells to permit standard  
 CC CC biochemical analysis. Overexpression of MDR-1 allows cytokine-driven

CC expansion of haematopoietic stem cells by at least 10-fold compared with  
 CC a maximum of 4-fold in known procedures  
 CC XX  
 CC SQ Sequence 3860 BP; 1135 A; 746 C; 957 G; 1022 T; 0 U; 0 Other;  
 CC  
 CC Query Match 100.0%; Score 25; DB 3; Length 3860;  
 CC Best Local Similarity 100.0%; Pred. No. 0.14;  
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 CGAACCGAGGCACTGCAATGGCGA 25  
 CC |||||  
 CC DB 1640 CGAACCGAGGCACTGCAATGGCGA 1616

Search completed: February 9, 2005, 16:05:59  
 Job time : 246.69 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: February 9, 2005, 13:42:02; Search time 266.667 Seconds  
(without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-14

Perfect score: 25  
Sequence: 1 CGAACCGAGGCGACGTGCATGCGCA 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgnt2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgnt2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgnt2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
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11: /cgnt2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgnt2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
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15: /cgnt2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
16: /cgnt2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
17: /cgnt2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
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21: /cgnt2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgnt2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	2307	9	US-09-805-020-31	Sequence 31, Appl
2	100.0	3825	17	US-10-363-112-48	Sequence 48, Appl
3	100.0	3840	18	US-10-384-339C-30	Sequence 30, Appl
4	100.0	3852	15	US-10-101-433A-1	Sequence 1, Appl
5	100.0	3860	9	US-09-866-866A-1	Sequence 1, Appl
6	100.0	3860	9	US-09-866-866A-3	Sequence 3, Appl
7	100.0	3924	9	US-09-880-107-2299	Sequence 2299, Ap
8	100.0	3924	17	US-10-641-643-1168	Sequence 1168, Ap
9	100.0	4186	17	US-10-619-359A-1	Sequence 1, Appl
10	100.0	4195	17	US-10-619-359A-3	Sequence 3, Appl
11	100.0	4533	9	US-09-805-020-30	Sequence 30, Appl

12	100.0	4643	13	US-10-072-621-2	Sequence 2, Appl
13	100.0	4643	15	US-10-097-340-1	Sequence 1, Appl
14	100.0	4643	14	US-10-007-925A-258	Sequence 258, App
15	100.0	4646	11	US-09-968-007A-459	Sequence 459, App
16	100.0	4646	11	US-09-968-007A-747	Sequence 747, App
17	100.0	4646	17	US-10-641-643-1167	Sequence 1167, App
18	100.0	4646	17	US-10-343-657-1	Sequence 1, Appl
19	100.0	4646	18	US-10-775-169-198	Sequence 198, App
20	100.0	4669	18	US-10-680-116-1	Sequence 1, Appl
21	100.0	8630	9	US-09-306-417-2	Sequence 2, Appl
22	100.0	8630	9	US-09-306-417-2	Sequence 1, Appl
23	87.2	4317	13	US-10-044-671-1	Sequence 1, Appl
24	87.2	4317	18	US-10-896-434-1	Sequence 1560, Ap
25	20.2	80.8	9	US-09-917-800A-1560	Sequence 5, Appl
26	20.2	80.8	4189	US-09-866-866A-5	Sequence 1424, Ap
27	20.2	80.8	4254	US-09-917-800A-1424	Sequence 265, App
28	20.2	80.8	4254	US-10-388-934-265	Sequence 1484, Ap
29	20.2	80.8	4254	US-10-152-319A-1484	Sequence 32, Appl
30	20.2	80.8	4298	US-10-335-053-32	Sequence 1, Appl
31	20.2	80.8	4369	US-09-769-097-1	Sequence 3, Appl
32	20.2	80.8	4425	US-09-769-097-3	Sequence 7, Appl
33	20.2	80.8	4788	US-09-866-866A-7	Sequence 33184, A
34	19.2	76.8	711	US-10-369-493-33184	Sequence 41419, A
35	19.2	76.8	747	US-10-369-493-41419	Sequence 59, Appl
36	19.2	76.8	7615	US-10-004-113-59	Sequence 4, Appl
37	19.2	76.8	55001	US-10-160-497-4	Sequence 4, Appl
38	19.2	76.8	55001	US-10-160-497-4	Sequence 1, Appl
39	19.2	76.8	2731748	US-10-297-465A-1	Sequence 38, Appl
40	19	76.0	19	US-10-016-490C-38	Sequence 29889, A
41	18.8	75.2	483	US-10-369-493-29889	Sequence 11, Appl
42	18.6	74.4	1175	US-09-873-409-11	Sequence 2443, Ap
43	18.6	74.4	1818	US-10-156-761-2443	Sequence 16, Appl
44	18.6	74.4	1940	US-09-873-409-16	Sequence 15, Appl
45	18.6	74.4	2021	US-09-873-409-15	

# ALIGNMENTS

RESULT 1  
US-09-805-020-31/c  
Sequence 31, Application US/09805020  
Publication No. US20020086384A1  
GENERAL INFORMATION:  
APPLICANT: LEVINE, Zuri  
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES  
FILE REFERENCE: 2786-0168P  
CURRENT APPLICATION NUMBER: US/09/805,020  
CURRENT FILING DATE: 2001-03-13  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)..(2307)  
OTHER INFORMATION: any n = a,c,g,t any unknown or other  
US-09-805-020-31

Query Match 100.0%; Score 25; DB 9; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 0.034; 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;

QY 1 CGAACCGAGGCGACGTGCATGCGCA 25  
DB 2064 CGAACCGAGGCGACGTGCATGCGCA 2040

RESULT 2  
US-10-363-112-48/c  
Sequence 48, Application US/10363112

Publication No. US20040091964A1  
GENERAL INFORMATION:  
APPLICANT: THE AUSTRALIAN NATIONAL UNIVERSITY  
APPLICANT: BOARD, PHILIP  
APPLICANT: HARRIS, MATTHEW  
TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF  
FILE REFERENCE: 007643-0302189  
CURRENT APPLICATION NUMBER: US/10/363,112  
CURRENT FILING DATE: 2003-11-03  
PRIOR APPLICATION NUMBER: PCT/AU01/01093  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: 60/229,663  
PRIOR FILING DATE: 2000-08-31  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 3825  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3825)  
US-10-363-112-48

Query Match 100.0%; Score 25; DB 17; Length 3825;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 1646 CGAACGAGGCGACGTGCAATGGCGA 1622

RESULT 3  
US-10-384-339C-30/C  
Sequence 30, Application US/10384339C  
Publication No. US20040175703A1  
GENERAL INFORMATION:  
APPLICANT: Kreutzer, Roland  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE  
FILE REFERENCE: 20200/2002  
CURRENT APPLICATION NUMBER: US/10/384,339C  
CURRENT FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: PCT/EP02/00152  
PRIOR FILING DATE: 2002-01-09  
PRIOR APPLICATION NUMBER: DE 10100586.5  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: DE 10155280.7  
PRIOR FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: DE 10158411.3  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: DE 10160151.4  
PRIOR FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 173  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 3840  
TYPE: DNA  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
TITLE: ndr-1  
PATENT DOCUMENT NUMBER: AF016535  
US-10-384-339C-30

Query Match 100.0%; Score 25; DB 18; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1637 CGAACGAGGCGACGTGCAATGGCGA 1613

RESULT 4  
US-10-101-433A-1/C  
Sequence 1, Application US/10101433A  
Publication No. US20030119726A1  
GENERAL INFORMATION:  
APPLICANT: Hanacom, Sara  
APPLICANT: Crespi, Charles  
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
FILE REFERENCE: G00307/70019  
CURRENT APPLICATION NUMBER: US/10/101,433A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: US 60/277,095  
PRIOR FILING DATE: 2001-03-19  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 3852  
TYPE: DNA  
ORGANISM: Macaca mulatta  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3852)  
US-10-101-433A-1

Query Match 100.0%; Score 25; DB 15; Length 3852;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 1649 CGAACGAGGCGACGTGCAATGGCGA 1625

RESULT 5  
US-09-866-866A-1/C  
Sequence 1, Application US/09866866A  
Patent No. US20020102244A1  
GENERAL INFORMATION:  
APPLICANT: Sorrentino, Brian  
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
FILE REFERENCE: 1340-1-021CIP2  
CURRENT APPLICATION NUMBER: US/09/866,866A  
CURRENT FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: 09/584,586  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: PCT/US99/11825  
PRIOR FILING DATE: 1999-05-27  
PRIOR APPLICATION NUMBER: 60/086,988  
PRIOR FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 3860  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 1640 CGAACGAGGCGACGTGCAATGGCGA 1616

RESULT 6  
US-09-866-866A-3/C  
Sequence 3, Application US/09866866A  
Patent No. US20020102244A1  
GENERAL INFORMATION:  
APPLICANT: Sorrentino, Brian



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; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-866-866A-3

Query Match          100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1640 CGAACCAGGCGCAGTGCATGGCGA 1616

RESULT 7
US-09-880-107-2299/c
; Sequence 2299, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2299
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M23234
; US-09-880-107-2299

Query Match          100.0%; Score 25; DB 9; Length 3924;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1678 CGAACCAGGCGCAGTGCATGGCGA 1654

RESULT 8
US-10-641-643-1168/c
; Sequence 1168, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cooke, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
```

```

; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9187501
; SEQUENCE DESCRIPTION: SEQ ID NO: 1168 :
US-10-641-643-1168

Query Match          100.0%; Score 25; DB 17; Length 3924;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGAACCAGGCGCAGTGCATGGCGA 25
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Db       1678 CGAACCAGGCGCAGTGCATGGCGA 1654

RESULT 9
US-10-619-359A-1/c
; Sequence 1, Application US/10619359A
; Publication No. US20040077000A1
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307.70020.US
; CURRENT APPLICATION NUMBER: US/10/619,359A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 09/672,810
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4186
; TYPE: DNA
; ORGANISM: Macaca fascicularis
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FEATURE:  
NAME/KEY: CDS  
LOCATION: (100)...(3940)  
US-10-619-359A-1

Query Match 100.0%; Score 25; DB 17; Length 4186;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 1739 CGAACGAGGCGACGTGCAATGGCGA 1715

RESULT 10  
US-10-619-359A-3/c  
Sequence 3, Application US/10619359A  
Publication No. US20040077000A1  
GENERAL INFORMATION:  
APPLICANT: STOCKER, PENNY J.  
APPLICANT: STEIMEL-CRESPI, DOROTHY T.  
APPLICANT: CRESPI, CHARLES L.  
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
FILE REFERENCE: G00307.70020.US  
CURRENT APPLICATION NUMBER: US/10/619,359A  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: US 60/156,921  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/158,818  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: US 09/672,810  
PRIOR FILING DATE: 2000-09-28  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 4195  
TYPE: DNA  
ORGANISM: Macaca fascicularis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (100)...(3949)  
US-10-619-359A-3

Query Match 100.0%; Score 25; DB 17; Length 4195;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 1748 CGAACGAGGCGACGTGCAATGGCGA 1724

RESULT 11  
US-09-805-020-30/c  
Sequence 30, Application US/09805020  
Publication No. US20020086384A1  
GENERAL INFORMATION:  
APPLICANT: LEVINE, Zurit  
TITLE OF INVENTION: SPICE VARIANTS OF ONCOGENES  
FILE REFERENCE: 2786-0168P  
CURRENT APPLICATION NUMBER: US/09/805,020  
CURRENT FILING DATE: 2001-03-13  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 4533  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(4533)  
OTHER INFORMATION: any n = a,c,g,t any unknown or other  
US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 2064 CGAACGAGGCGACGTGCAATGGCGA 2040

RESULT 12  
US-10-072-621-2/c  
Sequence 2, Application US/10072621  
Publication No. US20020169137A1  
GENERAL INFORMATION:  
APPLICANT: Reiner, Peter B.  
APPLICANT: Connop, Bruce P.  
APPLICANT: Pollard, Michelle  
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION  
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY  
FILE REFERENCE: 100103.402  
CURRENT APPLICATION NUMBER: US/10/072,621  
CURRENT FILING DATE: 2002-02-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 4643  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCAATGGCGA 25  
DB 2061 CGAACGAGGCGACGTGCAATGGCGA 2037

RESULT 13  
US-10-097-340-1/c  
Sequence 1, Application US/10097340  
Publication No. US20030087250A1  
GENERAL INFORMATION:  
APPLICANT: John MONAHAN  
APPLICANT: Manjula GANNANAPURU  
APPLICANT: Sebastian HORSCH  
APPLICANT: Shubhangi KAMATKAR  
APPLICANT: Steve G. KOVATS  
APPLICANT: Rachel E. MEYERS  
APPLICANT: Michael MORRISSEY  
APPLICANT: Peter OLANDT  
APPLICANT: Ami SEN  
APPLICANT: Peter VEIBY  
APPLICANT: Gordon B. MILLS  
APPLICANT: Robert C. BAST, Jr.  
APPLICANT: Karen LU  
APPLICANT: Rosemarie SCHMANDT  
APPLICANT: Xumei ZHAO  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer  
FILE REFERENCE: MRI-030  
CURRENT APPLICATION NUMBER: US/10/097,340  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 60/276,025  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/325,149  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/276,026  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/324,967

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; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-1

```

```

Query Match          100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CGAACGAGGCGCGTGCATGCGCA 25
Db      2061 CGAACGAGGCGCGTGCATGCGCA 2037

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RESULT 14
US-10-007-926A-258/c
; Sequence 258, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUIGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: atp-binding cassette, sub-family b
; OTHER INFORMATION: (mdr/cap), member 1 (ABCB1) gene.
US-10-007-926A-258

```

```

Query Match          100.0%; Score 25; DB 15; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 CGAACGAGGCGCGTGCATGCGCA 25
Db      2061 CGAACGAGGCGCGTGCATGCGCA 2037

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RESULT 15
US-09-968-007A-459/c
; Sequence 459, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Edner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02

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; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 459
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-459

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Query Match          100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CGAACGAGGCGCGTGCATGCGCA 25
Db      2064 CGAACGAGGCGCGTGCATGCGCA 2040

```

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Search completed: February 9, 2005, 22:26:42
Job time : 268.667 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds  
(without alignments)  
388.593 Million cell updates/sec

Title: US-10-007-255-14  
Perfect score: 25  
Sequence: 1 cgaaccaggcagcgtgcattgcgcga 25

Scoring table: IDENTITY NUC  
Gapop 10'-0', Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gsa1.\*  
9: gb\_gsa2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	290	7 F07318	F07318 HSC22A071 n
2	25	100.0	315	7 F08704	F08704 HSC22A021 n
3	25	100.0	320	7 F08211	F08211 HSC22C011 n
4	25	100.0	328	7 F06233	F06233 HSC11E051 n
5	25	100.0	357	7 T26505	T26505 AB282E2R In
6	25	100.0	469	7 R53330	R53330 Y983B02.r1
7	25	100.0	568	5 BP243819	BP243819 BP243819
8	25	100.0	570	5 BP220580	BP220580 BP220580
9	25	100.0	669	9 AG179058	AG179058 Pan trogl
10	25	100.0	699	9 AG179442	AG179442 Pan trogl
11	25	100.0	3843	9 AY408954	AY408954 Homo sapi
12	25	100.0	3843	9 AY408955	AY408955 Pan trogl
13	25	100.0	4035	3 BC042531	BC042531 Homo sapi
14	23.4	93.6	680	9 AG179392	AG179392 Pan trogl
15	20.2	80.8	360	1 AV191114	AV191114 AV191114
16	20.2	80.8	360	6 C12346	C12346 C12346 Yuij
17	20.2	80.8	374	1 AA789728	AA789728 vt78c08.r
18	20.2	80.8	485	6 CB727009	CB727009 AMGNRUC.N
19	20.2	80.8	550	4 BJ075336	BJ075336 BU075336
20	20.2	80.8	824	9 CC475658	CC475658 CH240_301
21	20.2	80.8	2792	3 AK050345	AK050345 Mus muscu
22	20.2	80.8	3182	3 AK030328	AK030328 Mus muscu
23	20.2	80.8	3816	9 AY408956	AY408956 Mus muscu
24	19.2	76.8	347	8 BZ840467	BZ840467 CH240_237

25	19.2	76.8	429	7 CF136217	CF136217 UI-HF-BN0
26	19.2	76.8	446	5 BQ343554	BQ343554 RCO-NT003
27	19.2	76.8	569	5 CR241012	CR241012 Reverse s
28	19.2	76.8	578	9 CE805931	CE805931 ligtr-gsa-
29	19.2	76.8	663	9 CN431062	CN431062 170005321
30	19.2	76.8	726	8 BH112888	BH112888 RPEC-24-2
31	19.2	76.8	754	7 CN431066	CN431066 170004245
32	19.2	76.8	845	4 BG818192	BG818192 602779778
33	19.2	76.8	3721	3 BC032414	BC032414 Homo sapi
34	18.8	75.2	392	1 A115290	A115290 uba87h07.r
35	18.8	75.2	580	2 BE687194	BE687194 uv94b10.y
36	18.8	75.2	638	1 AA175587	AA175587 ms95a01.r
37	18.8	75.2	639	7 CFS99341	CFS99341 NCST3d93
38	18.8	75.2	641	4 BJ814960	BJ814960 BJ814960
39	18.8	75.2	656	4 BJ818135	BJ818135 BJ818135
40	18.8	75.2	710	1 AA185993	AA185993 mc35b02.r
41	18.8	75.2	757	5 BU314758	BU314758 603544822
42	18.8	75.2	800	7 BG016473	CG14573 HRO4521_B
43	18.8	75.2	859	4 BG704400	BG704400 602687466
44	18.6	74.4	360	6 C67438	C67438 C67438 Yuij
45	18.6	74.4	375	6 C63703	C63703 C63703 Yuij

## ALIGNMENTS

RESULT 1  
LOCUS F07318 290 bp mRNA linear EST 20-FEB-1995  
DEFINITION HSC22A071 normalized infant brain cDNA Homo sapiens cDNA clone  
c-22a07, mRNA sequence.  
ACCESSION F07318 GI:672970  
VERSION F07318.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 290)  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
Devignes, M.D., Duprat, S., Houlgate, R., Junneau, M.N., Lamy, B.,  
Lorenzo, P., Mitchell, H., Marliage-Samson, R., Pletu, G., Poulliot, Y.,  
Sebastiani-Kabatchis, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome  
and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
95277534  
7757816  
Contact: Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpres@genethon.fr  
Single read.  
Genexpres\_library\_idc: C; Genexpres\_sequence\_idc: Y1c-22a07  
Seq primer: (-21)M13 universal.  
Location/Qualifiers  
1..290  
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/tissue\_type="total brain"  
/dev\_stage="3 months old"  
/clone\_lib="normalized infant brain cDNA"  
/note="Organ: brain; Vector: lambda B; Site 1: HindIII;  
Site 2: NotI; sex=female; dev\_stage=3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the

lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization\_method:  
Bento Soares, P.N.A.S in press"

## ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 290;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 CGAACCGAGGACGTCGCAATGGCGA 25  
|||||  
243 CGAACCGAGGACGTCGCAATGGCGA 267

## DB

RESULT 2  
LOCUS F08704 315 bp mRNA linear EST 21-FEB-1995  
DEFINITION HSCZ0A021 normalized infant brain CDNA Homo sapiens CDNA clone  
c-zoa02, mRNA sequence.  
ACCESSION F08704  
VERSION F08704.1 GI:6777708  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 315)  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B.,  
Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pietu, G., Pouillot, Y.,  
Sebastiani-Kabakchis, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome  
and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

## AUTHORS

## TITLE

JOURNAL  
MEDLINE  
PubMed  
95277534  
7757816

## COMMENT

Contact: Genethon  
Genexpress-Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpress@genethon.fr  
Single read.  
Genexpress library\_id: C; Genexpress\_sequence\_id: y2c-zoa02  
Seq primer: (-21)M13 universal.  
Location/Qualifiers  
1. 315  
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/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;  
Site 2: NotI; sex:Female; dev stages:3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dt) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization\_method:  
Bento Soares, P.N.A.S in press"

## FEATURES

## SOURCE

## ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.95;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 CGAACCGAGGACGTCGCAATGGCGA 25  
|||||  
243 CGAACCGAGGACGTCGCAATGGCGA 267

## DB

## RESULT 3

## LOCUS

F08211 320 bp mRNA linear EST 21-FEB-1995  
DEFINITION HSCZ0C011 normalized infant brain CDNA Homo sapiens CDNA clone  
c-zoc01, mRNA sequence.  
ACCESSION F08211  
VERSION F08211.1 GI:677727  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 320)  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B.,  
Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pietu, G., Pouillot, Y.,  
Sebastiani-Kabakchis, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome  
and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

## AUTHORS

## TITLE

JOURNAL  
MEDLINE  
PubMed  
95277534  
7757816

## COMMENT

Contact: Genethon  
Genexpress-Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpress@genethon.fr  
Single read.  
Genexpress library\_id: C; Genexpress\_sequence\_id: y1c-zoc01  
Seq primer: (-21)M13 universal.  
Location/Qualifiers  
1. 320  
/organism="Homo sapiens"  
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/sex="Female"  
/tissue\_type="total brain"  
/dev\_stage="3 months old"  
/clone\_lib="normalized infant brain CDNA"  
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;  
Site 2: NotI; sex:Female; dev stages:3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dt) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization\_method:  
Bento Soares, P.N.A.S in press"

## FEATURES

## SOURCE

## ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 320;  
Best Local Similarity 100.0%; Pred. No. 0.95;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 CGAACCGAGGACGTCGCAATGGCGA 25  
|||||  
243 CGAACCGAGGACGTCGCAATGGCGA 267

## DB

## RESULT 4

## LOCUS

F06233 328 bp mRNA linear EST 19-FEB-1995  
DEFINITION HSC11E051 normalized infant brain CDNA Homo sapiens CDNA clone  
c-11e05, mRNA sequence.  
ACCESSION F06233  
VERSION F06233.1 GI:670049  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 328)  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B.,  
Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pietu, G., Pouillot, Y.,  
Sebastiani-Kabakchis, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome  
and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PubMed

## COMMENT

## CONTACT

## GENEXPRESS

## GENETHON

## CENTRE

## DE RECHERCHE

## SUR LE

## GENOME

## HUMAIN

## 1, RUE DE

## L'INTERNATIONALE,

## BP60 91002

## EVRY CEDEx,

## FRANCE

## TEL: 33169472800

## FAX: 33160778698

## EMAIL: GENEXPRESS@GENETHON.FR

## SINGLE READ.

## GENEXPRESS

## LIBRARY\_ID: C;

## GENEXPRESS\_SEQUENCE\_ID: y1c-zoc01

## SEQ PRIMER: (-21)M13 UNIVERSAL.

## LOCATION/QUALIFIERS

## 1. 320

## /ORGANISM="Homo sapiens"

## /MOL\_TYPE="mRNA"

## /DB\_XREF="taxon:9606"

## /CLONE="c-zoc01"

## /SEX="Female"

## /TISSUE\_TYPE="total brain"

## /DEV\_STAGE="3 months old"

## /CLONE\_LIB="normalized infant brain CDNA"

## /NOTE="Organ: brain; Vector: lafmid BA; Site 1: HindIII;

## Site 2: NotI; sex:Female; dev stages:3 months old;

## isolate=muscular atrophy patient; tissue\_type=total

## brain; total mRNA was oligo-(dt) primed and directionally

## cloned 5' -&gt; 3' into the HindIII -&gt; NotI sites of the

## lafmid BA vector. Clone library from B.Souares, Psychiatry

## Dept. Columbia University, USA. Normalization\_method:

## Bento Soares, P.N.A.S in press"

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 328)  
Auffray, C., Behar, G., Bole, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houllgate, R., Juneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebasteian-Kabatchnik, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
9527534

JOURNAL  
MEDLINE  
PUBMED

7757816  
Contact: Genethon  
GeneXpress-Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33169778698  
Email: geneXpress@genethon.fr  
Single read.  
GeneXpress library\_id: C; GeneXpress\_sequence\_id: y1c-11e05  
Seq primer: (-21)M13 universal.

## FEATURES

## SOURCE

location/Qualifiers  
1..328  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="C-11e05"  
/sex="Female"  
/tissue\_type="total brain"  
/dev\_stage="3 months old"  
/clone\_lib="normalized infant brain cDNA"  
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII; Site 2: NotI; sex:Female; dev stage=3 months old; isolate=muscular atrophy patient; tissue type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Saeres, Psychiatry Dept. Columbia University, USA. Normalization\_method: Bento Soares, P.N.A.S in press"

## ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.95;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGAACCGGCGACGTGCATGGCGA 25  
Db 243 CGAACCGGCGACGTGCATGGCGA 267

## RESULT 5

LOCUS T26505 357 bp mRNA linear EST 15-APR-1996  
DEFINITION AB282E2R Infant brain, LNL array of Dr. M. Soares INTB Homo  
T26505 sapiens cDNA clone L1AB282E2 5', mRNA sequence.  
ACCESSION T26505  
VERSION T26505.1 GI:773822  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 357)  
Chico, N.S., Eveleth, G.G., Lfauellen, K. and Lennon, G.G.  
Infant brain cDNAs  
Genomics 28 (3), 570-572 (1995)  
96039272

JOURNAL  
MEDLINE  
PUBMED

7490096  
Contact: Greg G. Lennon  
Human Genome Center, L-452  
Lawrence Livermore National Laboratory  
Livermore CA 94550

FEATURES  
SOURCE

Tel: 510 422 8361  
Fax: 510 422 2282  
Email: info@image.llnl.gov  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..357  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="L1AB282E2"  
/clone\_lib="infant brain, LNL array of Dr. M. Soares  
INTB"  
/note="Vector: lafmid BA; Site 1: HindIII; Site 2: NotI; Normalized infant brain cDNA library made by Dr. M. Soares (Columbia University), oligo-dT primed and directionally cloned between HindIII (5') and NotI (3') sites "

## ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 357;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGAACCGGCGACGTGCATGGCGA 25  
Db 244 CGAACCGGCGACGTGCATGGCGA 268

## RESULT 6

LOCUS R53330 469 bp mRNA linear EST 18-MAY-1995  
DEFINITION YG83b02.r1 Soares infant brain INTB Homo sapiens cDNA clone  
IMAGE:39920 5', similar to gb:M23234 MULTIDRUG RESISTANCE PROTEIN 3  
(HUMAN), mRNA sequence.  
R53330  
EST.  
R53330.1 GI:815232

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 469)  
Hillier, L., Clark, N., Dubuque, T., Ellstrom, K., Hawkins, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Trevaekis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 2097  
High quality sequence stops: 371 Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 2097 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 371.  
Location/Qualifiers

TITLE  
JOURNAL  
COMMENTFEATURES  
SOURCE

1..469  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:412461"  
/db\_xref="taxon:9606"  
/clone="IMAGE:39920"  
/sex="female"  
/dev\_stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares infant brain INTB"  
/note="Organ: whole brain; Vector: lafmid BA; Site\_1: Not

I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5].  
 AACTGGAAGATTGGCCGACAGATTTTCTTTTCTTTT 3');  
 double-stranded cDNA was ligated to Hind III adaptor (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lambda B4 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 0.99;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGCATGCGCGCA 25  
 |||||  
 Db 242 CGAACGAGGCGCATGCGCGCA 266

## RESULT 7

BP243819/c 568 bp mRNA linear EST 15-SEP-2004  
 LOCUS BP243819 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone  
 DEFINITION BP243819 mRNA sequence.  
 ACCESSION BP243819  
 VERSION BP243819.1 GI:52116729  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 568)  
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
 TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions  
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
 COMMENT Department of Virology  
 Contact: Yutaka Suzuki  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
 Location/Qualifiers

## FEATURES

source 1..568  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HEP21483"  
 /issue\_type="liver"  
 /cell\_line="HepG2"  
 /clone\_lib="Sugano cDNA library, liver HepG2"  
 /note="hepatoma"

## ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 568;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGCATGCGCGCA 25  
 |||||  
 Db 156 CGAACGAGGCGCATGCGCGCA 132

## RESULT 8

BP220580/c 570 bp mRNA linear EST 15-SEP-2004  
 LOCUS BP220580 Sugano cDNA library, colon Homo sapiens cDNA clone  
 DEFINITION BP220580 mRNA sequence.  
 ACCESSION BP220580  
 VERSION BP220580.1 GI:52093485  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 570)  
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
 TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions  
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
 COMMENT Department of Virology  
 Contact: Yutaka Suzuki  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
 Location/Qualifiers

## FEATURES

source 1..570  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="COL03695"  
 /issue\_type="colon"  
 /clone\_lib="Sugano cDNA library, colon"

## ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGCATGCGCGCA 25  
 |||||  
 Db 245 CGAACGAGGCGCATGCGCGCA 221

## RESULT 9

AG179058/c 669 bp DNA linear GSS 09-JAN-2002  
 LOCUS AG179058 Pan troglodytes DNA, clone: RP43-051D12.T7, genomic survey  
 DEFINITION AG179058  
 ACCESSION AG179058  
 VERSION AG179058.1 GI:16708738  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes

## REFERENCE

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 TITLE BAC end sequences of library RP43-43  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 669)  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

## TITLE

Direct Submission  
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: schimpes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library RP43-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.  
 PRIMERS  
 Sequencing: T7  
 LIBRARY  
 Vector : pBac3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.  
 Location/Qualifiers

## FEATURES

source 1..669  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="RP43-051D12.T7"



ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 669;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGAACCGGCGCAGTGCATGCGCA 25  
162 CGAACCGGCGCAGTGCATGCGCA 138

RESULT 10  
AG179442/c 699 bp DNA linear GSS 09-JAN-2002  
DEFINITION Pan troglodytes DNA, clone: RP43-051112.T7, genomic survey  
SEQUENCE  
AG179442  
AG179442.1 GI:16709122  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toto, Y., Watanabe, H., and Sakaki, Y.  
BAC end sequences of Library RPCI-43  
Unpublished  
2 (bases 1 to 699)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toto, Y., Watanabe, H., and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Ageo Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimbee@res.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EORI  
R.Site 2 : EORI  
Location/Qualifiers  
1..699  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-051112.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 699;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGAACCGGCGCAGTGCATGCGCA 25  
150 CGAACCGGCGCAGTGCATGCGCA 126

RESULT 11  
AY408954/c 3843 bp DNA linear GSS 15-DEC-2003  
LOCUS AY408954/c  
DEFINITION Homo sapiens ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,

genomic survey sequence.  
AY408954  
AY408954.1 GI:39764922  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 3843)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 3843)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
1..3843  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
1..3843  
/gene="ABCB1"  
/locus\_tag="HCM3396"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGAACCGGCGCAGTGCATGCGCA 25  
1640 CGAACCGGCGCAGTGCATGCGCA 1616

RESULT 12  
AY408955/c 3843 bp DNA linear GSS 15-DEC-2003  
LOCUS AY408955/c  
DEFINITION Pan troglodytes ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY408955  
AY408955.1 GI:39764923  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 3843)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 3843)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source Location/Qualifiers  
1..3843  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..3843  
/gene="ABCB1"  
/locus\_tag="HGM3396"

ORIGIN  
Query Match 100.0%; Score 25; DB 9; Length 3843;  
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCAGGCGACGTGCATGGCGA 25  
1640 CGAACCAGGCGACGTGCATGGCGA 1616

Db

RESULT 13  
BC042531/c  
LOCUS Homo sapiens, ATP-binding cassette, sub-family B (MDR/TAP), member 4, clone IMAGE:4837724, mRNA.  
DEFINITION BC042531  
VERSION BC042531.1 GI:27503509  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 4035)  
Strausberg, R.  
Direct Submission  
Submitted (02-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnarsson, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

FEATURES  
source  
1..4035  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4837724"  
/tissue\_type="testis"  
/clone\_id="NH\_MGC\_97"  
/lab\_host="DH10B"

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAX Plate: 72 Row: 1 Column: 3  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9961253  
This clone has the following problem: frame shifted.

ORIGIN /note="Vector: pBluescript"

Query Match 100.0%; Score 25; DB 3; Length 4035;  
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCAGGCGACGTGCATGGCGA 25  
1758 CGAACCAGGCGACGTGCATGGCGA 1734

Db

RESULT 14  
AG179392/c  
LOCUS Pan troglodytes DNA, clone: RP43-051K1.17, genomic survey  
DEFINITION AG179392  
VERSION AG179392.1 GI:16709072  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library RPCT-43  
2 (bases 1 to 680)  
Unpublished  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenihiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: [chimpses@sc.riken.go.jp](mailto:chimpses@sc.riken.go.jp), URL: <http://hgp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library RPCT-43 This BAC end was generated during the Red process and may have higher chance of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBAC3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1..680  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-051K1.17"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_id="RPCT-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 93.6%; Score 23.4; DB 9; Length 680;  
Best Local Similarity 96.0%; Pred. No. 5.6; Indels 1; Gaps 0;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAACCAGGCGACGTGCATGGCGA 25  
125 CGAACCAGGCGACGTGCATGGCGA 101

Db

RESULT 15  
AV191114  
LOCUS 360 bp mRNA linear EST 22-JUL-1999  
DEFINITION AV191114 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone YK590b5 5', mRNA sequence.  
ACCESSION AV191114

SOURCE: Caenorhabditis elegans

ORGANISM  
Caenorhabditis elegans  
Eukaryote: Motile: No

Eukaryota; Metazoa; Metacoela; Ciliophorea; Rhaditida; Rhaditoidae; Rhaditidae; Peloderinae; Caenorhabditis.

REFERENCE  
AUTHORS  
1 (bases 1 to 360)  
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuiki, H.,

Nishigaki, A., Motomashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.

TITLE	Expressed genes in <i>C.elegans</i>
JOURNAL	Unpublished (1999)

COMMENT  
Contact: Yuji Kohara

Genome Biology Lab.  
National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp

FEATURES	Location/Qualifiers
source	1. .360

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/organism="Caenorhabditis elegans"
/mol_type="mRNA"
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/strain="N2"
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/day stages="embryo"
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/clone lib="Yuji Kohē
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hermaphrodite embryo"

## ORIGIN

Query match 80.8%; Score 20.2; DB 1; Length 360;

Best Local Similarity 88.0%; Pred. No. 1.5e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAACCGGGCAGCTGCAATGGCGA 25

Db 303 CGAACCAGGGCAGGTGAATGGAGA 327

Search completed: February 9, 2005, 21:55:45  
Job time : 2451.85 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds  
(without alignments)  
2517.530 Million cell updates/sec

Title: US-10-007-255-15

Perfect score: 25  
Sequence: 1 gctctgattccacgacactcctac 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_on:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_pl:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_rgs:\*  
12: gb\_by:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	AX504312	AX504312 Sequence
2	25	100.0	25	AX504329	AX504329 Sequence
3	25	100.0	210	HUMMDR1A14	M29435 Human P-gly
4	25	100.0	2726	I33621	I33621 Sequence 1
5	25	100.0	3840	AX481416	AX481416 Sequence
6	25	100.0	3840	BD171402	BD171402 Method fo
7	25	100.0	3860	AX322787	AX322787 Sequence
8	25	100.0	3860	AX322789	AX322789 Sequence
9	25	100.0	3988	BD190394	BD190394 Phosphat
10	25	100.0	3988	AX452556	AX452556 Sequence
11	25	100.0	3988	AX024454	AX024454 Sequence
12	25	100.0	4192	AF016535	AF016535 Homo sapi
13	25	100.0	4264	AR051647	AR051647 Sequence
14	25	100.0	4264	AR051650	AR051650 Sequence
15	25	100.0	4378	E02326	E02326 Multidrug r
16	25	100.0	4553	CO716151	CO716151 Sequence
17	25	100.0	4643	CO815440	CO815440 Sequence
18	25	100.0	4643	AX522070	AX522070 Sequence
19	25	100.0	4643	AX587788	AX587788 Sequence

c	20	25	100.0	4646	6	BD234195	BD234195 ATP-bind
c	21	25	100.0	4646	6	CO861565	CO861565 Sequence
c	22	25	100.0	4646	6	I49610	I49610 Sequence 2
c	23	25	100.0	4646	6	AR380622	AR380622 Sequence
c	24	25	100.0	4646	6	AX336420	AX336420 Sequence
c	25	25	100.0	4646	6	AX336708	AX336708 Sequence
c	26	25	100.0	4646	6	AX391099	AX391099 Sequence
c	27	25	100.0	4646	6	AX504298	AX504298 Sequence
c	28	25	100.0	4646	9	HUMMDR1	M14758 Homo sapien
c	29	25	100.0	4669	6	AX091275	AX091275 Sequence
c	30	25	100.0	4669	6	I08557	I08557 Sequence 3
c	31	25	100.0	4669	6	AR203322	AR203322 Sequence
c	32	25	100.0	4669	6	AR363344	AR363344 Sequence
c	33	25	100.0	4669	6	AR405961	AR405961 Sequence
c	34	25	100.0	6505	6	AR028671	AR028671 Sequence
c	35	25	100.0	8630	6	AR306491	AR306491 Sequence
c	36	25	100.0	8630	6	AR306492	AR306492 Sequence
c	37	25	100.0	8630	6	AX012320	AX012320 Sequence
c	38	25	100.0	8630	6	AX012321	AX012321 Sequence
c	39	25	100.0	9318	6	AR028672	AR028672 Sequence
c	40	25	100.0	98472	6	AX706975	AX706975 Sequence
c	41	25	100.0	98472	6	AX707905	AX707905 Sequence
c	42	25	100.0	98472	6	AC005068	AC005068 Homo sapi
c	43	25	100.0	128993	6	AX706983	AX706983 Sequence
c	44	25	100.0	128993	6	AX707913	AX707913 Sequence
c	45	25	100.0	147436	2	AC079303	AC079303 Homo sapi

#### ALIGNMENTS

RESULT 1  
AX504312  
LOCUS AX504312 25 bp DNA linear PAT 27-SEP-2002

DEFINITION Sequence 15 from Patent WO0234291.

ACCESSION AX504312

VERSION AX504312.1 GI:23386130

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Colgan, S.P.

AUTHORS Compositions and methods for treating hematologic malignancies and

TITLE multiple drug resistance

JOURNAL Patent: WO 0234291-A 15 02-MAY-2002;

FEATURES THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)

location/Qualifiers

1.25 /organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.04; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0;

Qy 1 GCTTGTGATCCACGACACTCCTAC 25

Db 1 GCTTGTGATCCACGACACTCCTAC 25

RESULT 2  
AX504329/c 25 bp DNA linear PAT 27-SEP-2002

DEFINITION Sequence 32 from Patent WO0234291.

ACCESSION AX504329

VERSION AX504329.1 GI:23386141

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 Colgan,S.P.

TITLE 1 Compositions and methods for treating hematologic malignancies and multiple drug resistance

JOURNAL THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)

FEATURES location/Qualifiers

source 1..25

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGATCCAGCAGCACTCTCTAC 25

Db 25 GCTTGATCCAGCAGCACTCTCTAC 1

RESULT 3 HUMMDR1A14/c 210 bp DNA linear PRI 08-JAN-1995

LOCUS Human P-glycoprotein (MDR1) gene, exon 16.

DEFINITION M29435.1 J05168

ACCESSION M29435.1 GI:187484

VERSION P-glycoprotein; multidrug resistance.

KEYWORDS 14 of 26

SEGMENT

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 210)

AUTHORS Chen,C.J., Clark,D., Ueda,K., Pastan,I., Gottesman,M.M. and Robinson,I.B.

TITLE Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoprotein

JOURNAL J. Biol. Chem. 265 (1), 506-514 (1990)

MEDLINE 90094448

PUBMED 1967175

COMMENT Original source text: Human multidrug resistant cell line KB-VL DNA.

Draft entry and computer-readable sequence for [1] kindly submitted by I.B.Robinson, 27-OCT-1989.

FEATURES Location/Qualifiers

source 1..210

/organism="Homo sapiens"

/mol\_type="genomic DNA"

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/map="7q21"

/gene="PGY1"

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prim\_transcript <1..>210

intron <1..17

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exon /note="PGY1, intron O"

18..194

/gene="PGY1"

/note="P-glycoprotein; G00-120-712"

/number=16

195..>210

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/note="PGY1, intron P"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGATCCAGCAGCACTCTCTAC 25

Db 160 GCTTGATCCAGCAGCACTCTCTAC 136

RESULT 4 133621 2726 bp DNA linear PAT 06-FEB-1997

LOCUS Sequence 1 from patent US 5593840.

DEFINITION 133621

ACCESSION 133621.1 GI:1824412

VERSION

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2726)

AUTHORS Bhatnagar,S.K., George,A.L., Jr. and Nazarenko,I.

TITLE Amplification of nucleic acid sequences

JOURNAL Patent: US 5593840-A 1 14-JAN-1997;

FEATURES location/Qualifiers

source 1..2726

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 2726;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGATCCAGCAGCACTCTCTAC 25

Db 534 GCTTGATCCAGCAGCACTCTCTAC 510

RESULT 5 AX481416 3840 bp DNA linear PAT 16-AUG-2002

LOCUS Sequence 30 from Patent WO02055693.

DEFINITION AX481416

ACCESSION AX481416

VERSION AX481416.1 GI:22316330

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Kreutzger,R., Limmer,S., Rost,S. and Hadwiger,P.

TITLE Method for inhibiting the expression of a target gene

JOURNAL Patent: WO 02055693-A 30 18-JUL-2002;

FEATURES Ribopharma AG (DE)

source 1..3840

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 3840;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGATCCAGCAGCACTCTCTAC 25

Db 2027 GCTTGATCCAGCAGCACTCTCTAC 2003

RESULT 6 BD171402 3843 bp DNA linear PAT 18-FEB-2003

LOCUS Method for predicting side effects of immunosuppressant and primer used therefor.

DEFINITION BD171402

ACCESSION BD171402.1 GI:28412692

VERSION

KEYWORDS	JP 2002223769-A/1.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 3843)
TITLE	Method for predicting side effects of immunosuppressant and primer used therefor
JOURNAL	Patent: JP 2002223769-A 1 13-AUG-2002;
COMMENT	SRL INC
OS	Homo sapiens (human)
PN	JP 2002223769-A/1
PD	13-AUG-2002
PF	31-JAN-2001 JP 2001024723
PI	ICHIRO IIRI
PC	C12N15/09, C12Q1/68, C12N15/00
CC	Method for predicting side effects of immunosuppressant and primer used
CC	therefor
FH	key
FT	Location/Qualifiers
FT	1. .3843
FT	Location/Qualifiers
FEATURES	source
ORIGIN	1. .3843
Query Match	100.0%; Score 25; DB 6; Length 3843;
Best Local Similarity	100.0%; Pred. No. 0.047;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GCTTGATTCACGACACTCTCTAC 25
DB	2030 GCTTGATTCACGACACTCTCTAC 2006
RESULT 7	AX322787/c
LOCUS	AX322787 3860 bp DNA linear PAT 07-JAN-2002
DEFINITION	Sequence 1 from Patent WO019287.
ACCESSION	AX322787
VERSION	AX322787.1 GI:18093766
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1
TITLE	Sorrentino, B. and Schuetz, J.
JOURNAL	Method of identifying and/or isolating stem cells
ST. JUDE	Patent: WO 019287-A 1 06-DEC-2001;
CHILDREN'S	RESEARCH HOSPITAL (US)
FEATURES	Location/Qualifiers
source	1. .3860
ORIGIN	1. .3860
Query Match	100.0%; Score 25; DB 6; Length 3860;
Best Local Similarity	100.0%; Pred. No. 0.047;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GCTTGATTCACGACACTCTCTAC 25
DB	2030 GCTTGATTCACGACACTCTCTAC 2006
RESULT 8	AX322789/c

LOCUS	AX322789	3860 bp	DNA	linear	PAT 07-JAN-2002
DEFINITION	Sequence 3 from Patent WO0192877.				
ACCESSION	AX322789				
VERSION	AX322789.1	GI:18093767			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 Scorrentino, B. and Schuetz, J. Method of identifying and/or isolating stem cells Patent: WO 0192877-A 3 06-DEC-2001; ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)				
FEATURES	Location/Qualifiers				
source	1..3860 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
ORIGIN					
Query Match	100.0%;	Score 25;	DB 6;	Length 3860;	
Best Local Similarity	100.0%;	Pred. No. 0.047;			
Matches	25;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	1 GCTTGTGATCCAGCAGACACTCTTAC 25       				
Db	2030 GCTTGTGATCCAGCAGACACTCTTAC 2006				
RESULT 9					
LOCUS	BD190394/c	3988 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Phosphatidylcholine as a medicament for the protection of mucosa.				
ACCESSION	BD190394				
VERSION	BD190394.1	GI:33000133			
KEYWORDS	JP 2002522381-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 3988)				
AUTHORS	Stremmel, W.				
TITLE	Phosphatidylcholine as a medicament for the protection of mucosa				
JOURNAL	Patent: JP 2002522381-A 1 23-JUL-2002; Wolfgang STREMMEI				
COMMENT	OS Homo Sapiens PN JP 2002522381-A/1 PD 23-JUL-2002 PF 06-AUG-1999 JP 2000563262 PR 06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DE 198 57 750.8 PT wolfgang stremmel				
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source	1..3988 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
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Query Match	100.0%;	Score 25;	DB 6;	Length 3988;	
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Matches	25;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	1 GCTTGTGATCCAGCAGACACTCTTAC 25       				
Db	2096 GCTTGTGATCCAGCAGACACTCTTAC 2072				
RESULT 10					
LOCUS	AR452556/c	3988 bp	DNA	linear	PAT 20-FEB-2004
LOCUS	AR452556				

DEFINITION Sequence 1 from patent US 6677319.  
ACCESSION AR452556  
VERSION AR452556.1 GI:42684344  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3988)  
AUTHORS Stremmel, W.  
TITLE Phosphatidylcholine as medication with protective effect large intestine  
JOURNAL Intestinal mucosa  
FEATURES Patent: US 6677319-A 1 13-JAN-2004;  
Location/Qualifiers  
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/organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 3988;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
Db 2096 GCTTGTGATCCAGCAGACTCTCTAC 2072

RESULT 11  
AX024454/c 3988 bp DNA linear PAT 15-SEP-2000  
LOCUS AX024454  
DEFINITION Sequence 1 from Patent DE19857750.  
ACCESSION AX024454  
VERSION AX024454.1 GI:10184622  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Stremmel, W.  
JOURNAL Patent: DE 19857750-A 1 24-FEB-2000;  
STREMMEL WOLFGANG (DE)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
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ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 3988;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
Db 2096 GCTTGTGATCCAGCAGACTCTCTAC 2072

RESULT 12  
AF016535/c 4192 bp mRNA linear PRI 03-SEP-1997  
LOCUS AF016535  
DEFINITION Homo sapiens P-glycoprotein (mdrl) mRNA, complete cds.  
ACCESSION AF016535  
VERSION AF016535.1 GI:2353263  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 4192)  
AUTHORS Chen, C.-U., Chin, J.-B., Ueda, K., Clark, D. P., Pastan, I., Gottesman, M. M. and Roninson, I. B.

TITLE Internal duplication and homology with bacterial transport proteins in the mdrl (P-glycoprotein) gene from multidrug-resistant human cells  
JOURNAL Cell 47 (3), 381-389 (1986)  
MEDLINE 87028230  
PUBMED 2876781  
REFERENCE 2 (bases 1 to 4192)  
AUTHORS Chen, G., Duran, G.E., Steger, K.A., Lacayo, N.J., Jaffrezou, J.P., Dumontet, C. and Sikic, B.I.  
TITLE Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein, altered phenotype, and resistance to cyclosporins  
JOURNAL J. Biol. Chem. 272 (9), 5974-5982 (1997)  
MEDLINE 97190336  
PUBMED 9038218  
REFERENCE 3 (bases 1 to 4192)  
AUTHORS Chen, G., Lacayo, N.J., Steger, K.A. and Sikic, B.I.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUL-1997) Medicine, Stanford University School of Medicine, Stanford, CA 94306, USA  
FEATURES Location/Qualifiers  
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/cell\_type="drug-resistant uterine sarcoma"  
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/note="multidrug-resistance gene"  
120..3959  
/gene="mdrl1"  
/function="transporter protein"  
/note="multidrug-resistance"  
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/protein\_id="AA069423.1"  
/db\_xref="GI:2353264"  
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WLDKLYMVVGTAAIIGHAGLPLMMVFESEMTDIFANAGNLDSMTNTRSDINDTG  
FPMNLEEDMTYAAVYVSGIGAGVLAAYQVSEFVLAAGROTHIKRPFHARBOEI  
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YKNLEEARIGIKKATITANSIGAEFLIYASVLAAPYQTTIVSGVSGICQUTV  
FVYLIGARVQASPSIEAFANRGAIEITKIDNKEIDSYSKSGKPRNKGKLE  
FNVHPSYSRREVKILKGLNKKVQSGVVALVNSGCKSTTVQLMQRLYDTEGVN  
SVNGODIRITNVRFLREIIGVSOEVPVFAITIAENIRGRBNVMTDETEKVEANA  
YDFIMKLPHKFPDLVGERGALSGGQKORIAIARALVRPKILLDEATSAIDTESEA  
VVOVALDKRKGRTTIVIAHRLSTVRNAVIGFDDGVVKGNDHLEKKEGITYFKL  
VMOTRAGNVELENAADESKRIIDALEMNSDNRSLIKRSTRBRVRSQADQVTS  
TKBALDESIPVPSFRINKLNTMPFVPGVFCALINGLDPAPRIITSKITGVTSR  
IDDPETKQNSNLFSLLFLALGITSFTFFLQGFPGKAGELITKRLRWRVRSMLRQ  
DVSFDDPKNITGALTTRLANDAAOVKAGISGRALVITININLIGTISFTYQOK  
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FEHMYAOSLOVPEYNSLRKAHIFGIFSTQTMAMFESVGCRRFAYVAHKLMSFD  
VILVFSAYVAGMAVGOVSFAADYAKAKITSAAHIMITEKPLIDSYSTEGMPTL  
EENVTGFEVENVPTRPDIPIVIOGSLBKKQOTLAVSSSGCGSTVQLLERFDP  
LAKKVLDDKEIKRLNVQMLRAHLGIVSOEPLTFQCSIAENIAYGDNSSVVOEETVR  
LAKENINAHFIESLPKRYSTKVGDKQTOISGGOKORIAARALVRPKILLDEATSA  
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3551

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Query Match 100.0%; Score 25; DB 9; Length 4192;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTTAC 25  
Db 2146 GCTTGTGATCCACGACACTCTTAC 2122

RESULT 13  
AR051647/c 4264 bp DNA linear PAT 29-SEP-1999

LOCUS AR051647  
DEFINITION Sequence 1 from patent US 5830697.  
ACCESSION AR051647  
VERSION AR051647.1 GI:5975011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4264)  
AUTHORS Slikic, B.I. and Chen, G.  
TITLE P-glycoprotein mutant resistant to cyclosporin modulation  
JOURNAL Patent: US 5830697-A 1 03-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..4264  
/organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTTAC 25  
Db 2168 GCTTGTGATCCACGACACTCTTAC 2144

RESULT 14  
AR051650/c 4264 bp DNA linear PAT 29-SEP-1999

LOCUS AR051650  
DEFINITION Sequence 5 from patent US 5830697.  
ACCESSION AR051650  
VERSION AR051650.1 GI:5975014  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4264)  
AUTHORS Slikic, B.I. and Chen, G.  
TITLE P-glycoprotein mutant resistant to cyclosporin modulation  
JOURNAL Patent: US 5830697-A 5 03-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..4264  
/organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTTAC 25  
Db 2168 GCTTGTGATCCACGACACTCTTAC 2144

RESULT 15  
E02326/c 4378 bp RNA linear PAT 29-SEP-1997  
LOCUS E02326  
DEFINITION Multidrug resistance relating gene derived from human normal cells.  
ACCESSION E02326  
VERSION E02326.1 GI:2170561  
KEYWORDS JP 1990100680-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 4378)  
AUTHORS Ueda, K. and Komano, T.  
TITLE HUMAN NORMAL CELL-DERIVED MDR RELATED GENE  
JOURNAL Patent: JP 1990100680-A 1 12-APR-1990;  
COMMENT SUNTOORY LTD

OS Homo sapiens  
PN JP 1990100680-A/1  
PD 12-APR-1990  
PF 05-OCT-1988 JP 1988251475  
PI UEDA KAZUMITSU, KOMANO TORU  
PC C12N15/12,C12N1/21,C12Q1/68;  
CC strandedness: Single;  
CC topology: Linear;  
CC \*source: tissue type=Adrenal gland;  
CC \*source: clone=5AM1132;  
FH Key Location/Qualifiers

FT 5'UTR 1..137  
FT CDS 138..3980  
FT FT /gene='Multidrug resistance relating gene' FT  
FT mat\_peptide 138..3977  
FT /gene='Multidrug resistance relating gene' FT

FEATURES  
source 1..4378  
/organism="Homo sapiens"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 4378;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTTAC 25  
Db 2167 GCTTGTGATCCACGACACTCTTAC 2143

Search completed: February 9, 2005, 17:02:02  
Job time : 481.178 secs



GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 : Search time 78.592 Seconds  
(without alignments)  
520.498 Million cell updates/sec

Title: US-10-007-255-15  
Perfect score: 25  
Sequence: 1 gcttgatccacgagcactccac 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCITUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	25	100.0	3988	4	US-09-762-195-1
C 3	25	100.0	4264	2	US-08-784-649A-1
C 4	25	100.0	4264	2	US-08-784-649A-5
C 5	25	100.0	4646	1	US-08-181-471-2
C 6	25	100.0	4646	4	US-09-023-655-1167
C 7	25	100.0	4659	2	US-08-752-447-1
C 8	25	100.0	4659	3	US-09-316-167-1
C 9	25	100.0	4659	4	US-09-397-233-1
C 10	25	100.0	4669	6	5206352-3
C 11	25	100.0	4669	6	5206352-3
C 12	25	100.0	6505	2	US-08-793-610-5
C 13	25	100.0	8630	4	US-09-306-417-1
C 14	25	100.0	8630	4	US-09-306-417-2
C 15	25	100.0	9318	2	US-08-793-610-6
C 16	24	96.0	4186	4	US-09-672-810-1
C 17	24	96.0	4195	4	US-09-672-810-3
C 18	23.4	93.6	4659	2	US-08-583-276-18
C 19	17.6	70.4	175236	4	US-09-949-016-1453
C 20	17	68.0	601	4	US-09-949-016-86814
C 21	17	68.0	606	4	US-09-252-991A-3463
C 22	17	68.0	1713	4	US-09-252-991A-3439
C 23	17	68.0	2112	4	US-09-252-991A-3494
C 24	17	68.0	2127	4	US-09-252-991A-3450
C 25	17	68.0	24204	4	US-09-949-016-16232
C 26	17	68.0	247781	4	US-09-949-016-1493
C 27	16.6	66.4	601	4	US-09-949-016-205911

28	16.6	66.4	601	4	US-09-949-016-205912	Sequence 205912, A
29	16.6	66.4	57761	4	US-09-949-016-13429	Sequence 13429, A
C 30	16.6	66.4	74644	4	US-09-949-016-17556	Sequence 17556, A
31	16.2	64.8	246	4	US-09-252-991A-11850	Sequence 11850, A
32	16.2	64.8	601	4	US-09-949-016-174875	Sequence 174875, A
33	16.2	64.8	601	4	US-09-949-016-174876	Sequence 174876, A
34	16.2	64.8	792	4	US-09-252-991A-11705	Sequence 11705, A
35	16.2	64.8	896	4	US-09-252-991A-11783	Sequence 11783, A
C 36	16.2	64.8	975	4	US-09-252-991A-11651	Sequence 11651, A
C 37	16.2	64.8	1083	4	US-09-252-991A-11533	Sequence 11533, A
38	16.2	64.8	16373	4	US-09-949-016-12820	Sequence 12820, A
C 39	16.2	64.8	16373	4	US-09-949-016-16887	Sequence 16887, A
C 40	16.2	64.8	45840	4	US-09-949-016-13903	Sequence 13903, A
C 41	16.2	64.8	45840	4	US-09-949-016-15042	Sequence 15042, A
C 42	16.2	64.8	46559	4	US-09-949-016-15043	Sequence 15043, A
C 43	16.2	64.8	49971	4	US-09-949-016-16668	Sequence 16668, A
44	16	64.0	19	4	US-08-820-479-6	Sequence 6, Appli
45	16	64.0	601	4	US-09-949-016-26189	Sequence 26189, A

## ALIGNMENTS

RESULT 1  
US-08-461-823-1/c  
Sequence 1, Application US/08461823  
Patent No. 5593840  
GENERAL INFORMATION:  
APPLICANT: Bhatnagar, Satish K.  
APPLICANT: George Jr., Albert L.  
APPLICANT: Nazarenko, Irina  
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACID SEQUENCES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESS: OncorPharm, Inc.  
STREET: 200 Perry Parkway  
CITY: Gaithersburg  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20877  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,823  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/168,621  
FILING DATE: 16-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/010,433  
FILING DATE: 27-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaita, Glenn E.  
REGISTRATION NUMBER: 30,649  
REFERENCE/DOCKET NUMBER: PA-0012 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301 527-2058  
TELEFAX: 301 208-6997  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2726 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-461-823-1

Query Match 100.0%; Score 25; DB 1; Length 2726;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCAGGACACTCTTAC 25  
Db 534 GCTTGTGATCCAGGACACTCTTAC 510

## RESULT 2

US-09-762-195-1/c  
Sequence 1, Application US/09762195  
Patent No. 6677319  
GENERAL INFORMATION:  
APPLICANT: Stremmel, Wolfgang  
TITLE OF INVENTION: Phosphatidylcholine as Medication with  
FILE REFERENCE: 34691/208520  
CURRENT FILING DATE: 2001-02-05  
PCT/EP9702426  
PRIOR FILING DATE: 1999-08-06  
PRIOR APPLICATION NUMBER: 198 35 526 2 DE  
PRIOR FILING DATE: 1998-08-06  
PRIOR APPLICATION NUMBER: 198 57 570.8 DE  
PRIOR FILING DATE: 1998-12-15  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FaesSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 3988  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-762-195-1

Query Match 100.0%; Score 25; DB 4; Length 3988;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCAGGACACTCTTAC 25  
Db 2096 GCTTGTGATCCAGGACACTCTTAC 2072

## RESULT 3

US-08-784-649A-1/c  
Sequence 1, Application US/08784649A  
Patent No. 5830697  
GENERAL INFORMATION:  
APPLICANT: Sikic, Branimir I  
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,649A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: Reg.No. 5830697 36,677  
REFERENCE/DOCKET NUMBER: 06037/007001

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4264 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-784-649A-1

Query Match 100.0%; Score 25; DB 2; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCAGGACACTCTTAC 25  
Db 2168 GCTTGTGATCCAGGACACTCTTAC 2144

## RESULT 4

US-08-784-649A-5/c  
Sequence 5, Application US/08784649A  
Patent No. 5830697  
GENERAL INFORMATION:  
APPLICANT: Sikic, Branimir I  
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,649A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: Reg.No. 5830697 36,677  
REFERENCE/DOCKET NUMBER: 06037/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4264 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCAGGACACTCTTAC 25  
Db 2168 GCTTGTGATCCAGGACACTCTTAC 2144

## RESULT 5

US-08-181-471-2/c  
 ; Sequence 2, Application US/08181471  
 ; Patent No. 5641508  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Lingna  
 ; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL  
 ; TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Thomas Fitting  
 ; STREET: 12526 High Bluff Drive, Suite 300  
 ; CITY: San Diego  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92130  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/181.471  
 ; FILING DATE: 13-JAN-1994  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/041,553  
 ; FILING DATE: 02-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fitting, Thomas  
 ; REGISTRATION NUMBER: 34,163  
 ; REFERENCE/DOCKET NUMBER: ANT0029P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-792-3680  
 ; TELEFAX: 619-792-8477  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4646 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 425..4267  
 ; US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
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 Db 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 6  
 US-09-023-655-1167/c  
 ; Sequence 1167, Application US/09023655.  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO

STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1167:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4646 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: g187468  
 ; US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
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 Db 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 7  
 US-08-752-447-1/c  
 ; Sequence 1, Application US/08752447  
 ; Patent No. 5994088  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mechtner, Eugene  
 ; APPLICANT: Robinson, Igor B  
 ; TITLE OF INVENTION: Methods and Reagents for Preparing and  
 ; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff Ltd.  
 ; STREET: 300 South Wacker Drive, Seventh Floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/752,447  
 ; FILING DATE: 15-NOV-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5994088nam, Kevin E  
 ; REGISTRATION NUMBER: 35,303  
 ; REFERENCE/DOCKET NUMBER: 95,1121

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-9808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4669 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

## RESULT 8

US-09-316-167-1/c

Sequence 1, Application US/09316167

Patent No. 6363357

GENERAL INFORMATION:

APPLICANT: Mechtner, Eugene

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and

USING IMMUNOLOGICAL AGENTS SPECIFIC FOR P-glycoprotein

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert &amp; Berghoff Ltd.

STREET: 300 South Wacker Drive, Seventh Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/316,167

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/752,447

ATTORNEY/AGENT INFORMATION:

FILING DATE: 15-NOV-1996

NAME: No. 6363357nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 95,1121

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-9808

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4669 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..424  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 425..4264  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 4265..4669  
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

## RESULT 9

US-09-397-233-1/c

Sequence 1, Application US/09397233

Patent No. 6630327

GENERAL INFORMATION:

APPLICANT: Mechtner, Eugene

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and

USING IMMUNOLOGICAL AGENTS SPECIFIC FOR P-glycoprotein

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert &amp; Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/397,233

FILING DATE: 16-Sep-1999

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: No. 6630327nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 95,1121-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4669 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..424

FEATURE:

NAME/KEY: CDS

LOCATION: 425..4264

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 4265..4669

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-397-233-1

Query Match 100.0%; Score 25; DB 4; Length 4669;

Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1 GCTGTGATCCAGCAGACTCTCTAC 25  
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 10  
5206352-3/c  
Patent No. 5206352  
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,  
Michael M.  
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/622,836  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 892,575  
FILING DATE: 01-AUG-1986  
APPLICATION NUMBER: 845,610  
FILING DATE: 28-MAR-1986  
SEQ ID NO:3:  
LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1 GCTGTGATCCAGCAGACTCTCTAC 25  
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 11  
5206352-3/c  
Patent No. 5206352  
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,  
Michael M.  
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA  
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/622,836  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 892,575  
FILING DATE: 01-AUG-1986  
APPLICATION NUMBER: 845,610  
FILING DATE: 28-MAR-1986  
SEQ ID NO:3:  
LENGTH: 4669  
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;  
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1 GCTGTGATCCAGCAGACTCTCTAC 25  
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 12  
US-08-793-610-5/c  
Sequence 5, Application US/08793610  
Patent No. 5858744  
GENERAL INFORMATION:  
APPLICANT: BAUM, Christopher  
APPLICANT: STOCKING-HARRERS, Carol

APPLICANT: OSTERTAG, Wolfram  
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF  
TITLE OF INVENTION: FOR GENE TRANSFER  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,610  
FILING DATE: 07-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 31 973.8  
FILING DATE: 08-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 03 952.1  
FILING DATE: 07-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03175  
FILING DATE: 10-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Berman, Richard J.  
REGISTRATION NUMBER: 39,105  
REFERENCE/DOCKET NUMBER: P1614-7007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
FAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6505 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA  
US-08-793-610-5

Query Match 100.0%; Score 25; DB 2; Length 6505;  
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1 GCTGTGATCCAGCAGACTCTCTAC 25  
DB 3846 GCTTGTGATCCAGCAGACTCTCTAC 3822

RESULT 13  
US-09-306-417-1/c  
Sequence 1, Application US/09306417  
Patent No. 6548301  
GENERAL INFORMATION:  
APPLICANT: Heinrich-Pette-Institut  
TITLE OF INVENTION: Retroviral Gene Transfer Vectors  
FILE REFERENCE: P50491  
CURRENT APPLICATION NUMBER: US/09/306,417  
CURRENT FILING DATE: 1999-05-06  
EARLIER APPLICATION NUMBER: DE 198 22 115  
EARLIER FILING DATE: 1998-05-08  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentlin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 8630  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: proviral

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/ OTHER INFORMATION: plasmid DNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(160)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (161)..(677)
/ OTHER INFORMATION: 5'-LTR
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: (532)..(1219)
/ FEATURE:
/ NAME/KEY: mac_peptide
/ LOCATION: (1220)..(5062)
/ OTHER INFORMATION: m4 mdr-1 cDNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5215)..(5774)
/ OTHER INFORMATION: 3'-LTR
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5775)..(8630)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(8630)
/ OTHER INFORMATION: retroviral expression vector SPbeta71m4
/ US-09-306-417-1
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Query Match          100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3249 GCTTGATCCAGGACGACCTCTAC 3225
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RESULT 14
US-09-306-417-2/c
/ Sequence 2, Application US/09306417
/ Patent No. 6548301
/ GENERAL INFORMATION:
/ APPLICANT: Heinrich-Pette-Institut
/ TITLE OF INVENTION: Retroviral Gene Transfer Vectors
/ FILE REFERENCE: P50491
/ CURRENT APPLICATION NUMBER: US/09/306,417
/ CURRENT FILING DATE: 1999-05-06
/ EARLIER APPLICATION NUMBER: DE 198 22 115
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 8630
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: proviral
/ OTHER INFORMATION: plasmid DNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(8630)
/ OTHER INFORMATION: retroviral expression vector SPbeta91MSAI
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(160)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (161)..(677)
/ OTHER INFORMATION: 5'-LTR
/ FEATURE:
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/ NAME/KEY: 5'UTR
/ LOCATION: (532)..(1219)
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/ LOCATION: (1220)..(5062)
/ OTHER INFORMATION: mSAI mdr1 cDNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5215)..(5774)
/ OTHER INFORMATION: 3'-LTR
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5775)..(8630)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ US-09-306-417-2
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Query Match          100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3249 GCTTGATCCAGGACGACCTCTAC 3225
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RESULT 15
US-08-793-610-6/c
/ Sequence 6, Application US/08793610
/ Patent No. 5858744
/ GENERAL INFORMATION:
/ APPLICANT: BAUM, Christopher
/ APPLICANT: STOCKING-HARRIS, Carol
/ APPLICANT: OSTERFAG, Wolfram
/ TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
/ TITLE OF INVENTION: FOR GENE TRANSFER
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Nikaïdo, Marmelstein, Murray & Oram LLP
/ STREET: 655 Fifteenth Street N.W. Suite 330
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/793,610
/ FILING DATE: 07-MAR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 44 31 973.8
/ FILING DATE: 08-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE 195 03 952.1
/ FILING DATE: 07-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03175
/ FILING DATE: 10-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Berman, Richard J.
/ REGISTRATION NUMBER: 39,105
/ REFERENCE/DOCKET NUMBER: P1614-7007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-5000
/ TELEFAX: (202)638-4810
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9318 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
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; MOLECULE TYPE: DNA  
US-08-793-610-6

Query Match 100.0%; Score 25; DB 2; Length 9318;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||  
Db 3805 GCTTGTGATCCAGACACTCTCTAC 3781

Search completed: February 9, 2005, 17:11:20  
Job time : 79.592 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds  
(Without alignments)  
539.601 Million cell updates/sec

Title: US-10-007-255-15

Perfect score: 15

Sequence: 1 gcttgcacacacgacacacacacac

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications NA: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	3840	US-10-384-339C-30	Sequence 30, Appl
2	25	100.0	3860	US-09-866-866A-1	Sequence 1, Appl
3	25	100.0	3860	US-09-866-866A-3	Sequence 3, Appl
4	25	100.0	4533	US-09-805-020-30	Sequence 30, Appl
5	25	100.0	4643	US-10-072-621-2	Sequence 2, Appl
6	25	100.0	4643	US-10-072-621-2	Sequence 1, Appl
7	25	100.0	4643	US-10-072-621-2	Sequence 258, App
8	25	100.0	4646	US-09-968-007A-459	Sequence 459, App
9	25	100.0	4646	US-09-968-007A-459	Sequence 747, App
10	25	100.0	4646	US-10-641-643-1167	Sequence 1167, App
11	25	100.0	4646	US-10-343-657-1	Sequence 1, Appl

12	25	100.0	4646	US-10-775-169-198	Sequence 198, App
13	25	100.0	4669	US-10-680-516-1	Sequence 1, Appl
14	25	100.0	8630	US-09-306-417-1	Sequence 1, Appl
15	25	100.0	8630	US-09-306-417-2	Sequence 2, Appl
16	24	96.0	3852	US-10-101-433A-1	Sequence 1, Appl
17	24	96.0	4186	US-10-619-359A-1	Sequence 1, Appl
18	24	96.0	4195	US-10-619-359A-3	Sequence 3, Appl
19	19.6	78.4	31	US-09-801-274-269	Sequence 269, App
20	17.6	70.4	34	US-10-425-115-130740	Sequence 130740, App
21	17.2	68.8	625	US-10-027-632-290365	Sequence 290365, App
22	17.2	68.8	625	US-10-027-632-290365	Sequence 290365, App
23	17.2	68.8	665	US-10-027-632-126989	Sequence 126989, App
24	17.2	68.8	665	US-10-027-632-126989	Sequence 126989, App
25	17.2	68.8	1005	US-10-369-493-26051	Sequence 26051, A
26	17.2	68.8	2390	US-10-027-632-101776	Sequence 101776, App
27	17.2	68.8	2390	US-10-027-632-101776	Sequence 101776, App
28	17.2	68.8	26555	US-09-860-670-161	Sequence 161, App
29	17.2	68.8	26555	US-10-227-646-161	Sequence 161, App
30	17.2	68.8	136328	US-10-101-510-127	Sequence 127, App
31	17.2	68.8	388	US-10-425-115-38049	Sequence 38049, A
32	17.2	68.0	463	US-10-027-632-70301	Sequence 70301, A
33	17.2	68.0	463	US-10-027-632-70301	Sequence 70301, A
34	17.2	68.0	550	US-10-027-632-36762	Sequence 36762, A
35	17.2	68.0	550	US-10-027-632-36762	Sequence 36762, A
36	17.2	68.0	762	US-09-938-842A-1088	Sequence 1088, App
37	17.2	68.0	942	US-10-384-842A-1088	Sequence 1088, App
38	17.2	68.0	1198	US-10-369-493-29334	Sequence 29334, A
39	17.2	68.0	1464	US-10-424-599-28742	Sequence 28742, A
40	17.2	68.0	1535	US-10-027-632-265708	Sequence 265708, App
41	17.2	68.0	1535	US-10-027-632-265708	Sequence 265708, App
42	17.2	68.0	1776	US-10-425-114-13600	Sequence 13600, A
43	17.2	68.0	1781	US-10-425-114-26722	Sequence 26722, A
44	17.2	68.0	1781	US-10-425-114-26722	Sequence 26722, A
45	17.2	68.0	1929	US-10-282-122A-23808	Sequence 23808, A

## ALIGNMENTS

RESULT 1  
US-10-384-339C-30/C  
Sequence 30, Application US/10384339C  
Publication No. US20040175703A1  
GENERAL INFORMATION:  
APPLICANT: Kreutzler, Roland  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GENE  
FILE REFERENCE: 20200/2002  
CURRENT FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: US/10/384,339C  
PRIOR FILING DATE: 2002-01-09  
PRIOR APPLICATION NUMBER: DE 1010586.5  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: DE 10155280.7  
PRIOR FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: DE 10158411.3  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: DE 10160151.4  
NUMBER OF SEQ ID NOS: 173  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 3840  
TYPE: DNA  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
TITLE: mdr-1  
PATENT DOCUMENT NUMBER: AF016535  
US-10-384-339C-30  
Query Match 100.0%; Score 25; DB 18; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGGACACTCCTAC 25  
DB 2027 GCTTGTGATCCAGGACACTCCTAC 2003

RESULT 2  
US-09-866-866A-1/c  
; Sequence 1, Application US/09866866A  
; Patent No. US20020102244A1  
; GENERAL INFORMATION:  
; APPLICANT: Sorrentino, Brian  
; APPLICANT: Schuetz, John  
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
; FILE REFERENCE: 1340-1-021CIP2  
; CURRENT APPLICATION NUMBER: US/09/866,866A  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 09/584,586  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: PCT/US99/11825  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: 60/086,988  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3860  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GCTTGTGATCCAGGACACTCCTAC 25  
DB 2030 GCTTGTGATCCAGGACACTCCTAC 2006

RESULT 3  
US-09-866-866A-3/c  
; Sequence 3, Application US/09866866A  
; Patent No. US20020102244A1  
; GENERAL INFORMATION:  
; APPLICANT: Sorrentino, Brian  
; APPLICANT: Schuetz, John  
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells  
; FILE REFERENCE: 1340-1-021CIP2  
; CURRENT APPLICATION NUMBER: US/09/866,866A  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 09/584,586  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: PCT/US99/11825  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: 60/086,988  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 3860  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-866-866A-3

Query Match 100.0%; Score 25; DB 9; Length 3860;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GCTTGTGATCCAGGACACTCCTAC 25  
DB 2030 GCTTGTGATCCAGGACACTCCTAC 2006

RESULT 4  
US-09-805-020-30/c  
; Sequence 30, Application US/09805020  
; Publication No. US20020086384A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, Zurit  
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES  
; FILE REFERENCE: 2786-0168P  
; CURRENT APPLICATION NUMBER: US/09/805,020  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 4533  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(4533)  
; OTHER INFORMATION: any n = a,c,g,t any unknown or other  
US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GCTTGTGATCCAGGACACTCCTAC 25  
DB 2454 GCTTGTGATCCAGGACACTCCTAC 2430

RESULT 5  
US-10-072-621-2/c  
; Sequence 2, Application US/10072621  
; Publication No. US20020169137A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiner, Peter B.  
; APPLICANT: Connop, Bruce P.  
; APPLICANT: Pollard, Michelle  
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION  
; FILE REFERENCE: 100103.402  
; CURRENT APPLICATION NUMBER: US/10/072,621  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 4643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GCTTGTGATCCAGGACACTCCTAC 25  
DB 2451 GCTTGTGATCCAGGACACTCCTAC 2427

RESULT 6  
US-10-097-340-1/c  
; Sequence 1, Application US/10097340  
; Publication No. US20030087250A1  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNAVAPU  
; APPLICANT: Sebastian HOERSCH  
; APPLICANT: Shubhangi KAMATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS

APPLICANT: Michael MORRISSEY  
APPLICANT: Peter OLANDT  
APPLICANT: Ami SEN  
APPLICANT: Peter VEIBY  
APPLICANT: Gordon B. MILLS  
APPLICANT: Robert C. BAST, Jr.  
APPLICANT: Karen LU  
APPLICANT: Rosemarie SCHMANDT  
APPLICANT: Xumel ZHAO  
APPLICANT: Karen GLATT  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer  
FILE REFERENCE: MRI-030  
CURRENT APPLICATION NUMBER: US/10/097,340  
PRIOR FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 60/276,025  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/325,149  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/276,026  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/324,967  
PRIOR FILING DATE: 2001/09/26  
PRIOR APPLICATION NUMBER: 60/311,732  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/325,102  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/323,580  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 363  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 4643  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-097-340-1

Query Match 100.0%; Score 25; DB 14; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
|||||  
Db 2451 GCTTGTGATCCAGCAGACTCTCTAC 2427

RESULT 7  
US-10-007-926A-258/c  
Sequence 258, Application US/10007926A  
Publication No. US20030143539A1  
GENERAL INFORMATION:  
APPLICANT: BERTUCCI, FRANCOIS  
APPLICANT: HOUTGATTE, REMI  
APPLICANT: BIRNBAUM, DANIEL  
APPLICANT: NGUYEN, CATHERINE  
APPLICANT: VIENS, PATRICE  
APPLICANT: FERRI, VINCENT  
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS  
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES  
FILE REFERENCE: 1546-R-00  
CURRENT APPLICATION NUMBER: US/10/007,926A  
PRIOR FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 60/254,090  
PRIOR FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 258  
LENGTH: 4643  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: acp-binding cassette, sub-family b  
OTHER INFORMATION: (mdr/cap), member 1 (ABCB1) gene.

US-10-007-926A-258

Query Match 100.0%; Score 25; DB 15; Length 4643;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
|||||  
Db 2451 GCTTGTGATCCAGCAGACTCTCTAC 2427

RESULT 8  
US-09-968-007A-459/c  
Sequence 459, Application US/09968007A  
Publication No. US20040115625A1  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa  
FILE REFERENCE: 689290-71  
CURRENT APPLICATION NUMBER: US/09/968,007A  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,172  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,173  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,278  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,294  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,295  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 1001  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 459  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-968-007A-459

Query Match 100.0%; Score 25; DB 11; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
|||||  
Db 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 9  
US-09-968-007A-747/c  
Sequence 747, Application US/09968007A  
Publication No. US20040115625A1  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa  
FILE REFERENCE: 689290-71  
CURRENT APPLICATION NUMBER: US/09/968,007A  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,172  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,173  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,278  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,294  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,295  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 1001  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 747  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-968-007A-747

PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 1001  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 747  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-968-007A-747

Query Match 100.0%; Score 25; DB 11; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGATCCAGCAGCACTCTAC 25  
DB 2454 GCTTGATCCAGCAGCACTCTAC 2430

## RESULT 10

US-10-641-643-1167/c  
Sequence 1167, Application US/10641643  
Publication No. US20040077003A1  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
Susan G. Stuart  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
GENE EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4646 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g187468  
SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :  
US-10-641-643-1167

Query Match 100.0%; Score 25; DB 17; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGATCCAGCAGCACTCTAC 25  
|||||

DB 2454 GCTTGATCCAGCAGCACTCTAC 2430

## RESULT 11

US-10-343-657-1/c  
Sequence 1, Application US/10343657  
Publication No. US20040086882A1  
GENERAL INFORMATION:  
APPLICANT: Roninson, Igor B.  
TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its  
ability to confer resistance to chemotherapeutic drugs  
FILE REFERENCE: 00,616-A  
CURRENT APPLICATION NUMBER: US/10/343,657  
CURRENT FILING DATE: 2003-10-17  
PRIOR APPLICATION NUMBER: 60/222,313  
PRIOR FILING DATE: 2000-08-01  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (425)..(4264)  
US-10-343-657-1

Query Match 100.0%; Score 25; DB 17; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGATCCAGCAGCACTCTAC 25  
DB 2454 GCTTGATCCAGCAGCACTCTAC 2430

## RESULT 12

US-10-775-169-198/c  
Sequence 198, Application US/10775169  
Publication No. US20040175743A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Burczynski, Michael  
APPLICANT: Twine, Natalie  
APPLICANT: Dornier, Andrew  
APPLICANT: Trepichio, William  
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
FILE REFERENCE: AM101080 (031896-013600)  
CURRENT APPLICATION NUMBER: US/10/775,169  
CURRENT FILING DATE: 2004-02-11  
NUMBER OF SEQ ID NOS: 5278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 198  
LENGTH: 4646  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-775-169-198

Query Match 100.0%; Score 25; DB 18; Length 4646;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGATCCAGCAGCACTCTAC 25  
DB 2454 GCTTGATCCAGCAGCACTCTAC 2430

## RESULT 13

US-10-680-516-1/c  
Sequence 1, Application US/10680516  
Publication No. US20040166110A1  
GENERAL INFORMATION:

```

APPLICANT: Mechtner, Eugene
            Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
            Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/680,516
FILING DATE: 07-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-680-516-1

Query Match      100.0%; Score 25; DB 18; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTGTGATCCACGACACTCTCTAC 25
Db      2454 GCTTGTGATCCACGACACTCTCTAC 2430

RESULT 14
US-09-306-417-1/c
Sequence 1, Application US/09306417
Patent No. US20020103144A1
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
```

```

SEQ ID NO 1
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (1220)..(5062)
OTHER INFORMATION: m4 mdr-1 cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SPbeta71m4
US-09-306-417-1

Query Match      100.0%; Score 25; DB 9; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTGTGATCCACGACACTCTCTAC 25
Db      3249 GCTTGTGATCCACGACACTCTCTAC 3225

RESULT 15
US-09-306-417-2/c
Sequence 2, Application US/09306417
Patent No. US20020103144A1
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
OTHER INFORMATION: plasmid DNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SPbeta91mSA1
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(160)
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; OTHER INFORMATION: plasmid backbone (puc)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (161)..(677)
; OTHER INFORMATION: 5'-LTR
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (532)..(1219)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1220)..(5062)
; OTHER INFORMATION: msA1 mdl1 cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5215)..(5774)
; OTHER INFORMATION: 3'-LTR
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5775)..(8630)
; OTHER INFORMATION: plasmid backbone (puc)
US-09-306-417-2
```

```
Query Match          100.0%; Score 25; DB 9; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTGATCCAGGACACTCTCTAC 25
Db      3249 GCTTGATCCAGGACACTCTCTAC 3225
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Search completed: February 9, 2005, 22:26:43  
Job time : 267.667 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds  
(Without alignments)  
602.360 Million cell updates/sec

Title: US-10-007-255-15  
Perfect score: 25  
Sequence: 1 gctctgcatccacgacgacacccctac 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6 AAD39004	Aad39004 Human mdr
2	25	100.0	25	6 AAD39014	Aad39014 Human mdr
3	25	100.0	594	10 ADK66076	Adk66076 Standardi
4	25	100.0	2726	2 AAO70907	Aao70907 Multidrug
5	25	100.0	2726	2 AAO70916	Aao70916 Multidrug
6	25	100.0	2726	2 AAT43322	Aat43322 Multidrug
7	25	100.0	3840	6 ABV78146	Abv78146 Human mdr
8	25	100.0	3840	6 ABZ35722	Abz35722 Human mdr
9	25	100.0	3840	6 ABX09965	Abx09965 Human mdr
10	25	100.0	3840	6 ABY19167	Abi19167 Human pol
11	25	100.0	3843	6 ABQ78185	Abq78185 Human MDR
12	25	100.0	3860	3 AAZ49332	Aaz49332 Human w11
13	25	100.0	3860	3 AAZ49333	Aaz49333 Human G18
14	25	100.0	3860	6 ABA94365	Abas94365 Human BCR
15	25	100.0	3860	6 ABA94366	Abas94366 Human BCR
16	25	100.0	3988	6 AAZ88973	Aaz88973 Human MDR
17	25	100.0	4264	2 AAV65533	Aav65533 Mutated h
18	25	100.0	4264	2 AAV65534	Aav65534 Mutated h
19	25	100.0	4349	4 AAH57442	Aah57442 Human int
20	25	100.0	4378	2 AAO45522	Aao45522 Multidrug

C 21	25	100.0	4533	6 ABS65229	Abas65229 cDNA enco
C 22	25	100.0	4643	6 ABS76368	Abas76368 cDNA enco
C 23	25	100.0	4643	6 ABV94267	Abv94267 Breast ca
C 24	25	100.0	4643	6 ABV74349	Abv74349 Human ABC
C 25	25	100.0	4643	10 ABX77217	Abx77217 cDNA enco
C 26	25	100.0	4643	12 ADP18689	Adp18689 Human MDR
C 27	25	100.0	4643	12 ADO19748	Ado19748 Human PRO
C 28	25	100.0	4643	13 ADP54881	Adp54881 Human PRO
C 29	25	100.0	4646	2 AAO72872	Aao72872 Human mdr
C 30	25	100.0	4646	3 AAZ94738	Aaz94738 Human ATP
C 31	25	100.0	4646	6 ABZ68592	Abz68592 Kidney ca
C 32	25	100.0	4646	6 ABZ68880	Abz68880 Kidney ca
C 33	25	100.0	4646	6 AAD38994	Adas38994 Human mdr
C 34	25	100.0	4646	10 ADK60994	Adk60994 Ovarian c
C 35	25	100.0	4646	11 ADI31841	Adi31841 Human CDN
C 36	25	100.0	4646	13 ADP52847	Adp52847 Drug ther
C 37	25	100.0	4669	1 AAN70752	Aan70752 Sequence
C 38	25	100.0	4669	2 AAQ52726	Aaq52726 Sequence
C 39	25	100.0	4669	2 AAV32645	Aav32645 Human P g
C 40	25	100.0	4669	6 ABK52041	Abk52041 cDNA enco
C 41	25	100.0	5544	13 ACNA3504	Acn33504 Human dia
C 42	25	100.0	6505	2 AAT13394	Aat13394 Hybrid ve
C 43	25	100.0	8630	3 AAZ22402	Aaz22402 Retrovira
C 44	25	100.0	8630	3 AAZ24041	Aaz24041 Retrovira
C 45	25	100.0	53099	6 ABS98185	Abas98185 Human mul

## ALIGNMENTS

RESULT 1	AAD39004	standard; DNA; 25 BP.
ID	AAD39004	standard; DNA; 25 BP.
XX	AAD39004;	
AC	23-SEP-2002	(first entry)
DT	23-SEP-2002	(first entry)
XX	Human mdr1-HRE antisense oligonucleotide #7.	
XX	Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;	
KW	hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;	
KW	lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;	
KW	myeloid disorder; lymphocytic leukaemia; thrombocytchaemia; myeloma;	
KW	angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;	
KW	polycythaemia vera; hypoxia responsive element; HRE; antisense;	
KW	phosphorothioate backbone; ss.	
OS	Homo sapiens.	
XX	Synthetic.	
FX	Key	Location/Qualifiers
FX	modified_base	1..25
FT	FT	/*tag= a
FT	FT	/mod_base= OTHER
FT	FT	/note= "phosphorothioate backbone"
XX	W0200234291-A2.	
XX	02-MAY-2002.	
XX	25-OCT-2001; 2001WO-US049856.	
XX	26-OCT-2000; 2000US-0243542P.	
XX	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.	
XX	Colgan SP;	
XX	WPI; 2002-471427/50.	
DR	Treating a subject (at risk of) having a hematologic malignancy or	
PT	multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia	

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
PT binding molecules.  
PS Claim 14; Page 43; 92pp; English.  
XX  
XX The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid  
CC disorders include chronic or acute myeloid leukaemia, e.g. angio-genic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is an antisense  
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its  
CC expression. This oligo is used in the exemplification of the invention  
XX  
SQ Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Gaps 0;  
Matches 25; Conservative 0; Indels 0; Gaps 0;  
QY 1 GCTTGTGATCCACGACACTCTTAC 25  
1 GCTTGTGATCCACGACACTCTTAC 25  
Db 1 GCTTGTGATCCACGACACTCTTAC 25  
RESULT 2  
AAD39014/c  
ID AAD39014 standard; DNA; 25 BP.  
XX  
XX AAD39014;  
AC  
XX 23-SEP-2002 (first entry)  
DT  
XX  
XX Human mdrl gene HIF-1 binding site DNA #7.  
DE  
XX  
XX Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;  
KM hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;  
KM lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;  
KM myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;  
KM angio-genic myeloid metaplasia; myeloid leukaemia; gene therapy;  
KM polycythaemia vera; hypoxia responsive element; HRE; ds.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT misc\_binding 11..15  
FT /\*tag= a  
FT /bound\_molety= "HIF-1"  
XX  
XX WO200234291-A2.  
PN  
XX  
XX 02-MAY-2002.  
PD  
XX 25-OCT-2001; 2001WO-US049856.  
PF  
XX 26-OCT-2000; 2000US-0243542P.  
PR  
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
PA  
XX Colgan SP;  
XX WPI; 2002-471427/50.  
XX  
XX Treating a subject (at risk of) having a hematologic malignancy or  
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia.

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1  
PT binding molecules.  
PS Example 2; Page 12; 92pp; English.  
XX  
XX The invention relates to a method of treating a subject having or at risk  
CC of developing a haematologic malignancy or multidrug resistance (MDR).  
CC The method involves administering hypoxia inducible factor-1 (HIF-1)  
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding  
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive  
CC element (HRE) binding molecules or antisense nucleic acid molecules and  
CC SUMO-1 binding molecules or antisense molecules are useful for treating a  
CC subject having or at risk of developing haematologic malignancy or MDR  
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders  
CC include lymphocytic leukemia or chronic lymphoproliferative disorders  
CC e.g. lymphoma, myeloma or chronic lymphoid leukemia. The myeloid  
CC disorders include chronic or acute myeloid leukemia, e.g. angio-genic  
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The  
CC invention is used in gene therapy. The present sequence is human mdrl  
CC gene HIF-1 binding site DNA  
XX  
SQ Sequence 25 BP; 6 A; 5 C; 9 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Gaps 0;  
Matches 25; Conservative 0; Indels 0; Gaps 0;  
QY 1 GCTTGTGATCCACGACACTCTTAC 25  
25 GCTTGTGATCCACGACACTCTTAC 1  
Db 25 GCTTGTGATCCACGACACTCTTAC 1  
RESULT 3  
ADK66076/c  
ID ADK66076 standard; RNA; 594 BP.  
XX  
XX ADK66076;  
AC  
XX 06-MAY-2004 (first entry)  
DT  
XX  
XX Standardized polynucleotide system polynucleotide #18.  
DE  
XX  
XX ss; standardized polynucleotide system; medical diagnosis;  
KM functional genomics; sample analysis; pharmacogenomics; sample analysis.  
XX  
XX Unidentified.  
OS  
XX DE10209071-A1.  
PN  
XX 25-SEP-2003.  
PD  
XX  
XX 28-FEB-2002; 2002DE-01009071.  
PF  
XX 28-FEB-2002; 2002DE-01009071.  
PR  
XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.  
PA  
XX Koehler T, Roest A;  
PI  
XX  
XX WPI; 2003-732912/70.  
DR  
XX  
XX Standardized polynucleotide system, useful for quantitative, real-time  
PT determination of nucleic acid, comprises stabilized standards, primers  
PT and probe.  
PS  
XX Claim 1; Page 12; 38pp; German.  
XX  
XX The present invention relates to a standardized polynucleotide system,  
CC which comprises at least one carrier nucleic acid, at least 3  
CC oligonucleotides, as primers and target-specific, fluorescently labeled  
CC probe and optionally at least one set of stabilized controls (standard  
CC RNA or DNA) of known concentration and instructions. The system comprises  
CC any of 20 sets of one control, two primers and one target-specific probe.

CC The standardized polynucleotide system can be used for quantitative, real  
CC -time detection of target nucleic acids, especially analysis of genes or  
CC gene products, e.g. for individualized medical diagnosis, in veterinary  
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,  
CC pharmaceutical testing, analysis of food or environmental samples and  
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present  
CC sequence is a polynucleotide used in the system of the invention.

XX Sequence 594 BP; 170 A; 125 C; 131 G; 0 T; 168 U; 0 Other;

Qy Query Match 100.0%; Score 25; DB 10; Length 594;  
Db Best Local Similarity 100.0%; Pred. No. 0.074;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCACGACACTCTCTAC 25  
Db 273 GCTTGTGATCCACGACACTCTCTAC 249

RESULT 4  
AAQ70907/c  
ID AAQ70907 standard; DNA; 2726 BP.

XX AAQ70907;  
XX 25-MAR-2003 (revised)  
DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

XX Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX W09417206-A1.

XX 04-AUG-1994.

XX 12-NOV-1993; 93WO-US010883.

XX 27-JAN-1993; 93US-00010433.

XX (ONCO-) ONCOR INC.

XX Bhattachar SK, George AL;

XX WPI, 1994-264118/32.

XX Enzymatic amplification of target nucleic acid sequences in a mixt. - to  
PT detect a mutation or allele in the target, e.g. that causes a genetic  
PT disease.

XX Disclosure; Page 30; 50pp; English.

XX This gene is used as an example of a target DNA in a method for the  
CC amplification of nucleic acid sequences in a mixture using various DNA  
CC probes/primers. The method may be used to detect a mutation or allele in  
CC the target, e.g. that causes a genetic disease. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

Qy Query Match 100.0%; Score 25; DB 2; Length 2726;  
Db Best Local Similarity 100.0%; Pred. No. 0.081;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCACGACACTCTCTAC 25  
Db 534 GCTTGTGATCCACGACACTCTCTAC 510

RESULT 5  
AAQ70916/c

ID AAQ70916 standard; DNA; 2726 BP.

XX AAQ70916;

XX 25-MAR-2003 (revised)

DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

XX Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX W09417210-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US000748.

XX 27-JAN-1993; 93US-00010433.

XX 16-DEC-1993; 93US-00168621.

XX (ONCO-) ONCOR INC.

XX Bhattachar SK, George AL;

XX WPI, 1994-264122/32.

XX Enzymatic amplification of target nucleic acid sequences to form exact or  
PT modified copies - has increased fidelity and can identify point mutations  
PT or allele(s).

XX Disclosure; Page 30; 69pp; English.

XX This gene is used as an example of a target DNA in a method for the  
CC amplification of nucleic acid sequences in a mixture using various DNA  
CC probes/primers. The method may be used to detect a mutation or allele in  
CC the target, e.g. that causes a genetic disease. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

Qy Query Match 100.0%; Score 25; DB 2; Length 2726;  
Db Best Local Similarity 100.0%; Pred. No. 0.081;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCACGACACTCTCTAC 25  
Db 534 GCTTGTGATCCACGACACTCTCTAC 510

RESULT 6

AAQ70916/c  
ID AAQ70916 standard; DNA; 2726 BP.

XX AAQ70916;

XX 01-SEP-1997 (first entry)

XX Multidrug resistance gene-1.

XX PCR, primer, amplify; polymerase chain reaction; ligase chain reaction;

XX LCR, human; multidrug resistance gene; MDR-1; ds.

XX Synthetic.

XX W09639537-A1.

XX 12-DEC-1996.

XX 04-JUN-1996; 96WO-US008841.

XX 05-JUN-1995; 95US-00461823.

XX (ONCO-) ONCOR INC.  
PA Bhatnagar SK, George AL, Nazarenko I;  
PI WPI; 1997-043158/04.  
XX  
XX Amplification method avoiding strand displacement by polymerase - used in  
PT the detection of mutation(s) and allele(s) associated with genetic  
PT disease and cancer.  
XX  
XX Example 1; Page 50-51; 92pp; English.  
XX  
XX This sequence represents the multidrug resistance gene (MDR-1) amplified  
CC by the primers shown in AAT43320 and AAT43321. This sequence can be used  
CC as a target in the method of the invention, for enzymatically amplifying  
CC a target nucleic acid (TNA) sequence contained in a nucleic acid or  
CC mixture of nucleic acids while avoiding strand displacement by  
CC polymerase. The method comprises using three primers, one complementary  
CC to a first segment of the TNA, a second complementary to a second segment  
CC of the TNA, which is adjacent to the first primer, and a third which is  
CC similar to the first segment of the TNA, and is complementary to a  
CC portion of the first primer. The first two primers are hybridised to the  
CC TNA, and a fused amplification product is created from the TNA using  
CC these two primers. The fused product is dissociated, and hybridised to  
CC the third primer, which is then extended. The extended modified  
CC amplification product is hybridised to the first two primers, and these  
CC two primers are ligated. Each of the primers may be labelled using a  
CC different label so that the method can be used to detect the presence of  
CC a mutation or allele by detecting whether the labelled primer is  
CC contained within the fused amplification product or the extended  
CC amplification product. The method of the invention combines certain  
CC aspects of ligase chain reaction (LCR) and polymerase chain reaction  
CC (PCR), but is improved compared to LCR due to the reduced number of  
CC primers needed, and the fact that the entire TNA sequence does not need  
CC to be known  
XX  
SQ Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 25; DB 2; Length 2726;  
XX Best Local Similarity 100.0%; Pred. No. 0.081;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GCTTGTGATCCAGGACACTCTCTAC 25  
XX |||||  
DB 534 GCTTGTGATCCAGGACACTCTCTAC 510  
XX  
RESULT 7  
ABV78146/c  
ID ABV78146 standard; DNA; 3840 BP.  
XX  
AC ABV78146;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human mdr-1 DNA SEQ ID NO 30.  
XX  
XX RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;  
KM virucide; protozoacide; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200255693-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EP000152.  
XX  
XX 09-JAN-2001; 2001DE-01000586.  
XX 26-OCT-2001; 2001DE-01055280.  
XX 29-NOV-2001; 2001DE-01058411.  
XX 07-DEC-2001; 2001DE-01060151.  
XX

XX (RIBO-) RIBOPHARMA AG.  
PA Kreutzer R, Limmer S, Rost S, Hadwiger P;  
PI WPI; 2002-590671/63.  
XX  
XX Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
PT target and having an overhang.  
XX  
XX Claim 10; Page 131-132; 203pp; German.  
XX  
XX The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in plasmodium or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression.  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention  
XX  
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 25; DB 6; Length 3840;  
XX Best Local Similarity 100.0%; Pred. No. 0.083;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GCTTGTGATCCAGGACACTCTCTAC 25  
XX |||||  
DB 2027 GCTTGTGATCCAGGACACTCTCTAC 2003  
XX  
RESULT 8  
ABZ35722/c  
ID ABZ35722 standard; DNA; 3840 BP.  
XX  
AC ABZ35722;  
XX  
DT 07-FEB-2003 (first entry)  
XX  
DE Human mdr-1 polynucleotide SEQ ID NO 30.  
XX  
XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;  
KM protozoacide; gene expression; antisense; tumour; infection; plasmodium;  
KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
KM Hepatitis C virus; human papilloma virus; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100588-A1.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2001; 2001DE-01000586.  
XX  
PR 09-JAN-2001; 2001DE-01000588.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
XX WPI; 2002-683450/74.  
XX  
XX Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are complementary  
PT to the target.  
XX  
PS Claim 13; Page 27-28; 100pp; German.  
XX

XX The invention relates to inhibiting expression of a target gene in a cell  
CC by introducing at least two oligoribonucleotides (dsRNA and IT), both  
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least one of one strand (S1, S2) of the ds structures in each  
CC of dsRNA and IT are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumours  
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is improved  
CC and efficiency can be increased further by pretreating the cells with  
CC interferon. The present sequence is that of a target DNA of the invention  
XX

SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. NO. 0.083;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
DB 2027 GCTTGTGATCCAGCAGACTCTCTAC 2003

RESULT 9  
ABX09965/c  
ID ABX09965 standard; DNA; 3840 BP.  
XX  
AC ABX09965;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Human mdr-1 DNA fragment SEQ ID 30.  
XX  
KM Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;  
KM prion; inhibition; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100587-Cl.  
XX  
PD 21-NOV-2002.  
XX  
PP 09-JAN-2001; 2001DE-01000587.  
XX  
PR 09-JAN-2001; 2001DE-01000587.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzler R, Limmer S, Rost S, Hadwiger P;  
XX  
DR WPI; 2002-742209/81.  
XX  
PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by  
XX introduction of complementary double-stranded oligoribonucleotide, after  
XX treating the cell with interferon.  
XX  
PS Disclosure; Page 32-33; 98pp; German.  
XX  
CC This invention describes a novel method for inhibiting expression of a  
CC target gene by introducing into the cell that contains the target gene at  
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)  
CC structure of not more than 49 consecutive nucleotides (nt), where at  
CC least a segment of one strand of the ds structure is complementary with  
CC the target gene and the cells are treated with interferon before  
CC introduction of dsRNA. The method is used to inhibit expression of  
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)  
CC protein genes, developmental or prion genes, or genes expressed in  
CC pathogenic organisms (particularly plasmodium) or in viruses or viroids  
CC (pathogenic in humans, animals or plants). Treating the cells with

CC interferon greatly increases the extent to which dsRNA can inhibit  
CC expression of the target genes, and the effect is even greater when dsRNA  
CC are modified to increase their stability. ABX09936-ABX10075 represent  
CC gene fragments used to illustrate the method of the invention  
XX

SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. NO. 0.083;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25  
DB 2027 GCTTGTGATCCAGCAGACTCTCTAC 2003

RESULT 10  
ABL91687/c  
ID ABL91687 standard; DNA; 3840 BP.  
XX  
AC ABL91687;  
XX  
DT 28-MAY-2002 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 30.  
XX  
KM Human, HIV, HCV, gene expression; oligoribonucleotide; tumour; pathogen;  
KM Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;  
KM cyostatic; virucide; protozoacide; antibacterial; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100586-Cl.  
XX  
PD 11-APR-2002.  
XX  
PP 09-JAN-2001; 2001DE-01000586.  
XX  
PR 09-JAN-2001; 2001DE-01000586.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzler R, Limmer S, Rost S, Hadwiger P;  
XX  
DR WPI; 2002-270454/32.  
XX  
PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by  
XX introducing double-stranded complementary oligoRNA having unpaired  
XX terminal bases.  
XX  
PS Claim 13; Page 28-30; 104pp; German.  
XX  
CC The invention relates to a method for inhibiting expression of a target  
CC gene (ABL91658-ABL91797) in a cell by introducing at least one  
CC oligoribonucleotide that has a double-stranded structure consisting of at  
CC most 49 sequential nucleotide pairs, with at least one end a single-  
CC complementary with the target gene and has at least one end a single-  
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for  
CC antisense inhibition of gene expression useful e.g. for treating tumours  
CC but the oligoribonucleotides may also be directed against genes present  
CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,  
CC animals or plants) or against cytokine, Id, developmental or prion genes.  
CC The method provides more effective inhibition of gene expression than use  
CC of known oligonucleotides, probably because the unpaired overhang  
CC increases stability and thus intracellular concentration  
XX

SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;  
Best Local Similarity 100.0%; Pred. NO. 0.083;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25

```
Db      2027 GCTTGTGATCCACGACACTCTCTAC 2003
|||||
RESULT 11
ABQ78185/c
ID      ABQ78185 standard; cDNA; 3843 BP.
XX
AC      ABQ78185;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Human MDR1 encoding cDNA SEQ ID NO 1.
XX
KM      Human; immunosuppressant; tacrolimus; cyclosporin; MDR1; SNP;
KM      single nucleotide polymorphism; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key          Location/Qualifiers
FT      CDS          1..3843
FT                      /*tag= a
FT                      /product= "MDR1"
FT      variation     replace(2677,A/T)
FT                      /*tag= b
FT                      /standart_name= "Single nucleotide polymorphism"
XX
PN      JP2002223769-A.
XX
PD      13-AUG-2002.
XX
PF      31-JAN-2001; 2001JP-00024723.
XX
PR      31-JAN-2001; 2001JP-00024723.
XX
PA      (SRLS-) SRL KK.
XX
DR      WPI; 2002-639348/69.
XX      P-PSDB; ABB83950.
XX
PT      Presuming the side effect of an immunosuppressant comprises using a
PT      primer set.
XX
PS      Disclosure; Page 6-11; 14pp; Japanese.
XX
CC      The invention relates to presumption of the side effect of at least one
CC      immunosuppressant selected from tacrolimus and cyclosporin in which if
CC      the 2677th base in the position of MDR1 gene in the encoding region of
CC      the cDNA sequence is guanine, adenine or thymine, is investigated. The
CC      method is used for the presumption of the side effect of an
CC      immunosuppressant. The present sequence is that of the MDR1 encoding cDNA
CC      of the invention
XX
SQ      Sequence 3843 BP; 1129 A; 740 C; 956 G; 1018 T; 0 U; 0 Other;
XX
Query Match          100.0%; Score 25; DB 6; Length 3843;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCTTGTGATCCACGACACTCTCTAC 25
DB      2030 GCTTGTGATCCACGACACTCTCTAC 2006
|||||
RESULT 12
AAZ49332/c
ID      AAZ49332 standard; cDNA; 3860 BP.
XX
AC      AAZ49332;
XX
DT      14-MAR-2000 (first entry)
XX
DE      Human wild-type multidrug resistance-1 (MDR-1) cDNA.
```

```
XX
KM      Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
KM      hematopoietic stem cell; transduction; bone marrow transplantation;
KM      chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
KM      genetic defect; thalassemia; Gauchier's disease; sickle cell anemia;
KM      leukemia; ex vivo expansion; cytokine; wild-type; ds.
XX
OS      Homo sapiens.
XX
FH      Key          Location/Qualifiers
FT      CDS          1..3843
FT                      /*tag= a
FT                      /product= "human wild-type MDR-1 protein"
FT      mutation     replace(553..555, GTT)
FT                      /*tag= b
FT                      /note= "cDNA sequence of G185V human mutant MDR-1 given
FT                      in AAZ49333"
XX
PN      .MO961589-A2.
XX
PD      02-DEC-1999.
XX
PF      27-MAY-1999; 99WC-US011825.
XX
PR      28-MAY-1998; 98US-0086988P.
XX
PA      (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PT      Sorrentino B, Bunting K;
XX
DR      WPI; 2000-072615/06.
XX      P-PSDB; AAY58186.
XX
PT      Ex vivo expansion of hematopoietic stem cells transduced with a sequence
PT      encoding human multidrug resistance-1, used for bone marrow
PT      transplantation.
XX
PS      Claim 10; Page 68-70; 113pp; English.
XX
CC      This sequence represents cDNA encoding human wild-type multidrug
CC      resistance protein MDR-1. MDR-1 is a transmembrane efflux pump,
CC      responsible for the export of drugs from cells, particularly cancer
CC      cells. Wild-type MDR-1 shows increased resistance to ecoposide and
CC      decreased resistance to vinca alkaloids compared with a mutant form
CC      (AAV58187) where the Gly at position 185 is replaced by Val. The
CC      invention relates to transducing hematopoietic stem cells with nucleic
CC      acid encoding an MDR protein and culturing the modified cells. The
CC      modified haematopoietic stem cells are useful in bone marrow
CC      transplantation (to reconstitute haematopoietic systems in patients who
CC      have undergone chemotherapy or radiation therapy) and in ex vivo gene
CC      therapy of genetic defects in cells derived from haematopoietic stem
CC      cells, e.g., thalassemia, Gauchier's disease, sickle cell anemia or
CC      leukemia. The modified cells can also be used to identify factors
CC      involved in regulating proliferation and differentiation in
CC      haematopoietic stem cells. Haematopoietic stem cells that express MDR-1
CC      will be protected against chemotherapeutic agents, so can be engrafted
CC      while the patient is undergoing chemotherapy. Expansion of (rare)
CC      hematopoietic stem cells provides sufficient cells to permit standard
CC      biochemical analysis. Overexpression of MDR-1 allows cytokine-driven
CC      expansion of haematopoietic stem cells by at least 10-fold compared with
CC      a maximum of 4-fold in known procedures
XX
SQ      Sequence 3860 BP; 1135 A; 746 C; 957 G; 1022 T; 0 U; 0 Other;
XX
Query Match          100.0%; Score 25; DB 3; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCTTGTGATCCACGACACTCTCTAC 25
DB      2030 GCTTGTGATCCACGACACTCTCTAC 2006
|||||
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XX	RESULT 13
XX	AAZ49333/C
XX	ID AAZ49333 standard; cDNA; 3860 BP.
XX	AC
XX	AAZ49333;
DT	14-MAR-2000 (first entry)
DE	
XX	Human G185V mutant multidrug resistance-1 (MDR-1) cDNA.
XX	Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
KW	haematopoietic stem cell; transplantation; bone marrow transplantation;
KW	chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
KM	genetic defect; thalassemia; Gaucher's disease; sickle cell anaemia;
KW	leukaemia; ex vivo expansion; cytokine; mutant; da.
XX	
OS	Synthetic.
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
CDS	1..3843
FT	/*tag= A
FT	/product= "Human G185V mutant MDR-1 protein"
PN	MO9961589-A2.
PD	
XX	02-DEC-1999.
PF	27-MAY-1999; 99WO-US011825.
XX	
FR	28-MAY-1998; 98US-0086988P.
XX	
PA	(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PI	
XX	Sorrentino B, Bunting K;
DR	WPI; 2000-072615/06.
DR	P-PSDB; AAY58187.
XX	
PT	Ex vivo expansion of hematopoietic stem cells transduced with a sequence
PT	encoding human multidrug resistance-1, used for bone marrow
PT	transplantation.
PS	
XX	Example 1; Page 79-82; 113pp; English.
CC	This sequence represents cDNA encoding human G185V mutant multidrug
CC	resistance protein MDR-1, where the Gly residue at position 185 of the
CC	wild-type protein (AAY58186) is replaced by Val. MDR-1 is a transmembrane
CC	efflux pump, responsible for the export of drugs from cells, particularly
CC	cancer cells. The wild-type MDR-1 shows increased resistance to etoposide
CC	and decreased resistance to vinca alkaloids compared with the G185V
CC	mutant. The invention relates to transducing haematopoietic stem cells
CC	with nucleic acid encoding an MDR protein and culturing the modified
CC	cells. The modified haematopoietic stem cells are useful in bone marrow
CC	transplantation (to reconstitute haematopoietic systems in patients who
CC	have undergone chemotherapy or radiation therapy) and in ex vivo gene
CC	therapy of genetic defects in cells derived from haematopoietic stem
CC	cells, e.g. thalassemia, Gaucher's disease, sickle cell anaemia or
CC	leukemia. The modified cells can also be used to identify factors
CC	involved in regulating proliferation and differentiation in
CC	haematopoietic stem cells. Haematopoietic stem cells that express MDR-1
CC	will be protected against chemotherapeutic agents, so can be engrafted
CC	while the patient is undergoing chemotherapy. Expansion of (rare)
CC	haematopoietic stem cells provides sufficient cells to permit standard
CC	biochemical analysis. Overexpression of MDR-1 allows cytokine-driven
CC	expansion of haematopoietic stem cells by at least 10-fold compared with
CC	a maximum of 4-fold in known procedures
XX	
SQ	Sequence 3860 BP; 1135 A; 746 C; 956 G; 1023 T; 0 U; 0 Other;
Query Match	100.0%; Score 25; DB 3; Length 3860;
Best Local Similarity	100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0	

[illegible]

## RESULT 15

ABA94366/C  
ID ABA94366 standard; DNA; 3860 BP.

XX ABA94366;

XX 26-MAR-2002 (first entry)

XX Human BCRP DNA related seq Id No. 3.

XX Stem cell; ATP transport protein; ATP-binding cassette; antiparkinsonian;  
XX hepatocytic; neurodegenerative; cytosolic; antianemic; muscular; BCRP;  
XX cardiac; gene therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3843  
FT /\*tag= a

XX WO200192877-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001WO-US017459.

XX 31-MAY-2000; 2000US-00584586.

XX 29-MAY-2001; 2001US-00866866.

XX (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Sorrentino B, Schuetz J;

XX WPI; 2002-114368/15.

XX P-PSDB; ABB07267.

XX Identifying a stem cell, for treating e.g., muscular dystrophy,  
PT myocardial infarction, Parkinson's disease, or neurodegenerative  
PT disorders, comprises detecting the expression of an ATP transport protein  
PT (BCRP) by a cell.

XX Disclosure; Page 59-60; 87pp; English.

XX The invention provides a method of identifying and/or isolating a stem  
CC cell that involves detecting the expression of an ATP transport protein  
CC containing a conserved ATP-binding cassette (BCRP) by a cell in a sample  
CC comprising stem cells. The isolated stem cells may be used in the  
CC treatment of diseases such as muscular dystrophy, degenerative liver  
CC disorder, myocardial infarction, Parkinson's disease, degenerative  
CC disorders of the brain, and for tissue regeneration or replacement.  
CC Haematopoietic cells can be used in bone marrow transplants (e.g., for  
CC treatment of leukemia) and for ex vivo gene therapy for treating blood  
CC diseases such as sickle cell anemia and thalassemia. The stem cells can  
CC also be used as cell targets in gene therapy protocols. The present  
CC sequence represents a sequence related to the BCRP for which no relevant  
CC information has been provided in the specification

XX Sequence 3860 BP; 1135 A; 746 C; 956 G; 1023 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 6; Length 3860;

XX Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCACGACACTCTTAC 25

Db 2030 GCTTGTGATCCACGACACTCTTAC 2006

Search completed: February 9, 2005, 16:05:59  
Job time : 245.69 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds  
(Without alignments)  
388.593 Million cell updates/sec

Title: US-10-007-255-15

Perfect score: 1 gcttgatccacgacactcctac 25

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hlc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_g981.\*  
9: gb\_g982.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	568	5	BP243819 BP243819
2	25	100.0	579	5	BP242809 BP242809
3	25	100.0	3843	9	AY408954 Homo sapi
4	25	100.0	3843	9	AY408955 Pan trogl
5	22	88.0	497	5	BX645450 DKFZp781C
6	20.8	83.2	534	4	BM414475 EST01407
7	20.8	83.2	569	5	BX317766 BX317766
8	20.8	83.2	574	5	BX320207 BX320207
9	20.8	83.2	588	6	CA058097 ssalngae51
10	20.8	83.2	592	5	CA044923 ssalngae00
11	20.8	83.2	595	5	BX310867 BX310867
12	20.8	83.2	619	5	BX868539 BX868539
13	20.8	83.2	623	6	CA052009 ssalngae53
14	20.8	83.2	642	7	CR369095 CR369095
15	20.8	83.2	657	6	CB507124 ssalob505
16	20.8	83.2	658	5	BX317788 BX317788
17	20.8	83.2	691	6	CA040401 ssalhc50
18	20.8	83.2	701	7	CR375818 CR375818
19	20.8	83.2	729	6	CA055205 ssalngae54
20	20.8	83.2	747	5	BX875171 BX875171
21	20.8	83.2	755	5	BX871907 BX871907
22	20.8	83.2	773	5	BX884053 BX884053
23	20.8	83.2	773	5	BX884541 BX884541
24	20.8	83.2	782	5	BX320208 BX320208

C	25	20.8	83.2	792	5	BX861388	BX861388
	26	20.2	80.8	688	5	BU478361	BU478361
	27	20.2	80.8	726	8	BH704692 BOMG53TF	BH704692
	28	19.2	76.8	547	5	BX874038	BX874038
	29	19.2	76.8	692	6	CB509048	CB509048
	30	19.2	76.8	728	7	CR362263	CR362263
	31	19.2	76.8	912	9	CL208918	CL208918
	32	18.8	75.2	641	4	BJ699561	BJ699561
	33	18.8	75.2	645	4	BJ676814	BJ676814
	34	18.8	75.2	650	4	BJ533210	BJ533210
	35	18.8	75.2	650	4	BJ700611	BJ700611
	36	18.8	75.2	661	1	AU091247	AU091247
	37	18.8	75.2	661	4	BJ014564	BJ014564
	38	18.8	75.2	764	4	BJ505685	BJ505685
	39	18.8	75.2	786	4	BJ720789	BJ720789
	40	18.8	75.2	830	7	CN986052	CN986052
	41	18.8	75.2	853	7	CN986052	CN986052
	42	18.8	75.2	856	7	CN986052	CN986052
	43	18.8	75.2	856	7	CN977721	CN977721
	44	18.8	75.2	858	7	CN987415	CN987415
	45	18.8	75.2	1011	4	BJ740383	BJ740383

#### ALIGNMENTS

RESULT 1  
BP243819/c 568 bp mRNA linear EST 15-SEP-2004  
LOCUS BP243819 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone  
DEFINITION HEP21483, mRNA sequence.  
ACCESSION BP243819  
VERSION BP243819.1 GI:52116729  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,  
Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
Genome Res. 14 (9), 1711-1718 (2004)  
JOURNAL Contact: Yutaka Suzuki  
COMMENT Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.  
FEATURES  
source location/Qualifiers  
1..568  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="HEP21483"  
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/cell\_line="HepG2"  
/clone\_id="Sugano cDNA library, liver HepG2"  
/note="Hepatooma"  
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Best Local Similarity 100.0%; Pred.No. 0.56; 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GCTTGTGATCCACGACACTCCTAC 25  
DB 546 GCTTGTGATCCACGACACTCCTAC 522  
RESULT 2  
BP242809/c 579 bp mRNA linear EST 15-SEP-2004  
LOCUS BP242809

DEFINITION	BP242809 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
ACCESSION	HEP17994, mRNA sequence.
VERSION	BP242809
KEYWORDS	BP242809.1 GI:52115719
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 579)
TITLE	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
JOURNAL	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
COMMENT	Genome Res. 14 (9), 1711-1718 (2004)
FEATURES	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8659, Japan Email: yusuzuki@ims.u-tokyo.ac.jp. Location/Qualifiers
source	1..579 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="HEP17994" /issue_type="liver" /cell_line="HepG2" /clone_id="Sugano cDNA library, liver HepG2" /note="hepatoma"
ORIGIN	
Query Match	100.0%; Score 25; DB 5; Length 579;
Best Local Similarity	100.0%; Pred. No. 0.56;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCTGTGATCCAGCAGCACTCTTAC 25 
Db	252 GCTGTGATCCAGCAGCACTCTTAC 228
RESULT 3	
AY408954/c	3843 bp DNA linear GSS 15-DEC-2003
LOCUS	AY408954
DEFINITION	Homo sapiens ABCB1 gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY408954
VERSION	AY408954.1 GI:39764922
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 3843)
TITLE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
JOURNAL	Infering nonneutral evolution from human-chimp-mouse orthologous gene trics
COMMENT	Science 302 (5657), 1960-1963 (2003)
FEATURES	14671302 2 (bases 1 to 3843) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment. Location/Qualifiers

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source
1. .3843
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/mol_type="genomic DNA"
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<1. .>3843
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGATCCACGACACTCTCTAC 25
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|||||

Db 2030 GCTGTGATCCACGACACTCTCTAC 2006

RESULT 4
AY408955/c 3843 bp DNA linear GSS 15-DEC-2003
LOCUS
DEFINITION
Pan troglodytes ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY408955
VERSION
AY408955.1 GI:39764923
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 3843)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smrnsky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene tris
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 3843)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smrnsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment
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1. .3843
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGATCCACGACACTCTCTAC 25
|||||
|||||

Db 2030 GCTGTGATCCACGACACTCTCTAC 2006

RESULT 5
BX645450/c 497 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION
BX645450
DKFZp781c1343_r1 781 (synonym: h1cc4) Homo sapiens cDNA clone
DKFZp781c1343 5', mRNA sequence.

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**ACCESSION** BX645450  
**VERSION** BX645450.1 GI:34479783  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**AUTHORS** 1 (bases 1 to 497)  
 Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
 Mewes, H.W., Weill, B., Amid, C., Oanger, A., Fodor, G., Han, M. and  
 Wiemann, S.  
 EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,  
 Wellenreuther, R., et al.)  
 Unpublished (2003)  
**JOURNAL** Contact: MIPS  
**COMMENT** MIPS  
 Ingolsteedter Landstr.1, D-85764 Neuberg, Germany  
 This is the 5' sequence of the clone insert  
 clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
 sequenced by DKFZ (German Cancer Research Center,  
 Heidelberg/Germany) within the CDNA sequencing consortium of the  
 German Genome Project.  
 No 81 sequence available.  
 This clone (DKFZp781C1343) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
**FEATURES** Location/Qualifiers  
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 /lab\_host="DH10B"  
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**ORIGIN**  
 Query Match 88.0%; Score 22; DB 5; Length 497;  
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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 GCTTGATCCACGACACTCC 22  
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 22 GCTTGATCCACGACACTCC 1

**Db** 22 GCTTGATCCACGACACTCC 1

**RESULT 6**  
 BM414475 534 bp mRNA linear EST 01-JAN-2004  
**LOCUS** EST01407 Atlantic salmon Lambda Zap Express ovary cDNA library  
**DEFINITION** Salmo salar cDNA clone oyr\_004\_d08 5', mRNA sequence.  
**ACCESSION** BM414475  
**VERSION** BM414475.1 GI:40542222  
**KEYWORDS** EST.  
**SOURCE** Salmo salar (Atlantic salmon)  
**ORGANISM** Salmo salar  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Proacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 1 (bases 1 to 534)  
 Caplice, N.C., Martin, S.A., Davey, G.C. and Powell, R.  
 An expressed sequence tag-based list of genes expressed in the  
 testis and ovary of Atlantic salmon (Salmo salar)  
 Unpublished (2002)  
**JOURNAL** Contact: Caplice NC  
**COMMENT** Department of Microbiology  
 National University of Ireland Galway (NUIG)  
 National University of Ireland Galway, Galway, Ireland  
 Tel: 00353 91 524411 2254  
 Fax: 00353 91 525700

Email: nicole.caplice@nui.galway.ie  
 Insert Length: 535 Std Error: 0.00  
 Plate: ovary rare plate 4 row: d column: 08  
 Seq primer: M13 reverse primer = caggaatacgtatgacc  
 High quality sequence scop: 535  
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 /clone\_lib="Atlantic salmon Lambda Zap Express ovary cDNA  
 library"  
 /note="Organ: ovary; Vector: Lambda Zap Express; Site 1:  
 EcoRI; Site 2: XhoI; An Atlantic salmon ovary cDNA library  
 was constructed using the Lambda Zap Express/Gigapack  
 cloning kit (Stratagene cloning systems). cDNA synthesis  
 was carried out using an oligo (dT) primer for the  
 reverse transcription of 5ug of mRNA and the library was  
 constructed by directional cloning EcoRI-XhoI based on  
 manufacturers instructions. An insert:vector ligation  
 ratio of 1:5 was chosen as most optimum. The lambda  
 library was packaged with Gigapack III gold packaging  
 extracts and plated on the E. coli cell line XL1-Blue  
 MRF."

**ORIGIN**  
 Query Match 83.2%; Score 20.8; DB 4; Length 534;  
 Best Local Similarity 91.7%; Pred. No. 56;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 2 CTTGTGATCCACGACACTCTAC 25  
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 356 CTTGTGATCCACGACACTCTAC 333

**Db** 356 CTTGTGATCCACGACACTCTAC 333

**RESULT 7**  
 BX317766 569 bp mRNA linear EST 14-MAY-2004  
**LOCUS** BX317766 tcay Oncorhynchus mykiss cDNA clone tcay0033b.p.22 3prtm.  
**DEFINITION** mRNA sequence.  
**ACCESSION** BX317766  
**VERSION** BX317766.2 GI:40308402  
**KEYWORDS** EST.  
**SOURCE** Oncorhynchus mykiss (rainbow trout)  
**ORGANISM** Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 569)  
 Govoroun, M., Guiguen, Y. and Le Gac, F.  
 Construction and primary characterization of normalized cDNA  
 libraries in rainbow trout, Oncorhynchus mykiss  
 Unpublished (2003)  
**JOURNAL** On Apr 7, 2003 this sequence version replaced gi:29598411.  
**COMMENT** Contact: Guiguen Y  
 INRA - SCRIBE  
 Campus de Beaulieu, RENNES cedex, 35042, France  
 Tel: 02.23.48.50.09  
 Fax: 02.23.48.50.20  
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us  
 at eigenasupport@jouy.inra.fr to obtain the chromatogram of this  
 sequence.  
 Plate: 0033 row: p column: 22  
 Seq primer: M13F.  
**FEATURES** Location/Qualifiers  
**source** 1..569  
 /organism="Oncorhynchus mykiss"

/mol\_type="mRNA"  
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 /clone="tcay003b.p.22"  
 /tissue\_type="adipose tissue, blood, brain,  
 differentiating gonads, gills, interrenal, intestine,  
 kidney, liver, muscle, ovary, pituitary, testis"  
 /dev\_stage="from embryos to adults"  
 /lab\_host="DH10B"  
 /clone\_lib="tcay"  
 /note="Vector: pT73D-pac; Rainbow trout multi-tissues -  
 normalized + 1 subtraction (tcay); Clone distribution :  
 AGENAS Resource centre, Francois Piumi,  
 Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et  
 Etude du genome (LREG), Domaine de Vilvert, 78352,  
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33  
 (0) 1.34.65.22.73"

ORIGIN  
 Query Match 83.2%; Score 20.8; DB 5; Length 569;  
 Best Local Similarity 91.7%; Pred. No. 56;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGGACACTCTCTAC 25  
 |||||||  
 Db 385 CTTGTGATCCAGGACACTCTCTAC 362

RESULT 8  
 BX320207/c 574 bp mRNA linear EST 20-MAY-2004  
 LOCUS BX320207 tcay Oncorhynchus mykiss cDNA clone tcay003b.a.22 3prim,  
 DEFINITION mRNA sequence.  
 ACCESSION BX320207  
 VERSION BX320207.2 GI:40309605  
 KEYWORDS EST.  
 SOURCE Oncorhynchus mykiss (rainbow trout)  
 ORGANISM Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 574)  
 Govoroun,M., Guiguen,Y. and le Gac,F.  
 Construction and primary characterization of normalized cDNA  
 libraries in rainbow trout, Oncorhynchus mykiss  
 Unpublished (2003)  
 On Apr 7, 2003 this sequence version replaced gi:29600852.  
 JOURNAL  
 COMMENT Contact: Guiguen Y  
 INRA - SCRIBE  
 Campus de Beaulieu, RENNES cedex, 35042, France  
 Tel: 02.23.48.50.09  
 Fax: 02.23.48.50.20  
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us  
 at aigenasupport@jouy.inra.fr to obtain the chromatogram of this  
 sequence.  
 Plate: 0038 row: a column: 22  
 Seg primer: M13F.  
 location/Qualifiers  
 1..574  
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 /clone="tcay003b.a.22"  
 /tissue\_type="adipose tissue, blood, brain,  
 differentiating gonads, gills, interrenal, intestine,  
 kidney, liver, muscle, ovary, pituitary, testis"  
 /dev\_stage="from embryos to adults"  
 /lab\_host="DH10B"  
 /clone\_lib="tcay"  
 /note="Vector: pT73D-pac; Rainbow trout multi-tissues -  
 normalized + 1 subtraction (tcay); Clone distribution :  
 AGENAS Resource centre, Francois Piumi,  
 Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et

Etude du genome (LREG), Domaine de Vilvert, 78352,  
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33  
 (0) 1.34.65.22.73"

ORIGIN  
 Query Match 83.2%; Score 20.8; DB 5; Length 574;  
 Best Local Similarity 91.7%; Pred. No. 56;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGGACACTCTCTAC 25  
 |||||||  
 Db 328 CTTGTGATCCAGGACACTCTCTAC 305

RESULT 9  
 CA058097 568 bp mRNA linear EST 04-MAR-2003  
 LOCUS 98a1rga513143 mixed\_tissue Salmo salar cDNA, mRNA sequence.  
 ACCESSION CA058097  
 VERSION CA058097.1 GI:24388340  
 KEYWORDS EST.  
 SOURCE Salmo salar (Atlantic salmon)  
 ORGANISM Salmo salar  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Proacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 1 (bases 1 to 568)  
 GRASP Consortium, Davidson,W.S., Koop,B.F. and  
 http://web.uvic.ca/cbr/grasp.  
 A survey of Salmo salar transcripts from high complexity cDNA  
 libraries  
 Unpublished (2002)  
 JOURNAL  
 COMMENT Centre for Biomedical Research  
 University of Victoria  
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
 Tel: 250 472 4067  
 Fax: 250 472 4075  
 Email: bkoop@uvic.ca  
 Genome Sciences Centre, BC Cancer Agency  
 cDNA preparation, sequencing and bioinformatics:  
 Y Butterfield, R Kirkpatrick, J Asano, N Gilm, R Guin, D Lee,  
 S Lee, T Olson, P Pandoh, A Prabhu, D Smallus, L Spence, J Stott,  
 S Taylor, G Yang, J Schein, S Jones and M Marra.  
 location/Qualifiers  
 1..568  
 /organism="Salmo salar"  
 /mol\_type="mRNA"  
 /strain="McConnell"  
 /db\_xref="taxon:8030"  
 /clone\_lib="mixed tissue"  
 /note="Vector: pCIVSsport6; Library Creator: Research  
 Genetics; Atlantic salmon tissue contributors: Carlo  
 Biagi, Mitch Un and Robert Devlin (DFO, Vancouver, B.C.),  
 Simon Jones (PBS, Nanaimo, B.C.), Seaspriing Hatchery  
 (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN  
 Query Match 83.2%; Score 20.8; DB 6; Length 588;  
 Best Local Similarity 91.7%; Pred. No. 56;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGGACACTCTCTAC 25  
 |||||||  
 Db 256 CTTGTGATCCAGGACACTCTCTAC 279

RESULT 10  
 CA044923 592 bp mRNA linear EST 04-MAR-2003  
 LOCUS 98a1mg6003036 gut Salmo salar cDNA, mRNA sequence.  
 DEFINITION CA044923  
 ACCESSION CA044923  
 VERSION CA044923.1 GI:24349786

**KEYWORDS**  
EST.  
Salmo salar (Atlantic salmon)

**SOURCE**  
Salmo salar

**ORGANISM**  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

**REFERENCE**  
1 (bases 1 to 592)  
GRASP Consortium, Davidson, W.S., Koop, B.F. and  
http://web.uvic.ca/cdr/grasp.  
A survey of Salmo salar transcripts from high complexity cDNA libraries

**TITLE**  
Unpublished (2002)

**JOURNAL**  
Contact: Koop BF  
Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Centre for Biomedical Research, University of Victoria  
cDNA preparation and sequencing:  
Roberto Alberto, Marianne Beetz-Sargent, Maura Busby,  
Peter Hunt, Linda McKinnel, BF Koop.  
bioinformatics:  
Gordon D Brown.

**FEATURES**  
Source  
1..592  
/organism="Salmo salar"  
/mol\_type="mRNA"  
/db\_xref="taxon:8030"  
/clone\_lib="gut"  
/note="Vector: pBluescriptIIK+; Library Creator: Matthew L. Rise; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seasing Hatcher (Crofton, B.C.), Rachel Roper (University of Victoria)."

**ORIGIN**  
Query Match 83.2%; Score 20.8; DB 6; Length 592;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY**  
2 CTTGTGATCCAGCAGCACTCTCTAC 25  
|||||  
41 CTTGTGATCCAGCAGCACTCTCTAC 18

**Db**  
2 CTTGTGATCCAGCAGCACTCTCTAC 25  
|||||  
41 CTTGTGATCCAGCAGCACTCTCTAC 18

**RESULT 11**  
BX910867/c 595 bp mRNA linear EST 27-JUL-2004  
DEFINITION  
BX910867 tcdk Oncorhynchus mykiss cDNA clone tcdk0072c.m.23 5prim,  
mRNA sequence.  
BX910867  
BX910867.2 GI:43435782  
EST.  
Oncorhynchus mykiss (rainbow trout)  
Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 595)  
Govoroun, M., Guiguen, Y. and Le Gac, F.  
Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss  
Unpublished (2003)  
On Jan 22, 2004 this sequence version replaced gi:41127666.  
Contact: Guiguen Y  
INRA - SCRIBE  
Campus de beaulieu, RENNES cedex, 35042, France  
Tel: 02.23.48.50.09  
Fax: 02.23.48.50.20  
Email: Yann.Guiguen@beaulieu.rennes.inra.fr

**JOURNAL**  
COMMENT

Sequence cleaned of vector, adaptor and repetitions. Contact us at [sigenasupport@jouy.inra.fr](mailto:sigenasupport@jouy.inra.fr) to obtain the chromatogram of this sequence.  
Plate: 0072 row: m column: 23  
Seq primer: M13R.

**FEATURES**  
Source  
1..595  
/organism="Oncorhynchus mykiss"  
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/db\_xref="taxon:8032"  
/clone="tcdk0072c.m.23"  
/cissue\_type="multi-issues"  
/dev\_stage="from embryos to adults"  
/lab\_host="DH10B"  
/clone\_lib="tcdk"  
/note="Vector: pT73D-pac; AGENAE Rainbow trout multi-issues - normalized + 2 subtractions; Clone distribution: AGENAE Resource centre, Francois PUMI, Francois Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

**ORIGIN**  
Query Match 83.2%; Score 20.8; DB 5; Length 595;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY**  
2 CTTGTGATCCAGCAGCACTCTCTAC 25  
|||||  
484 CTTGTGATCCAGCAGCACTCTCTAC 461

**Db**  
2 CTTGTGATCCAGCAGCACTCTCTAC 25  
|||||  
484 CTTGTGATCCAGCAGCACTCTCTAC 461

**RESULT 12**  
BX868539/c 619 bp mRNA linear EST 24-MAY-2004  
DEFINITION  
BX868539 tcdk Oncorhynchus mykiss cDNA clone tcdk0027c.1.14 5prim,  
mRNA sequence.  
BX868539  
BX868539.2 GI:42777807  
EST.  
Oncorhynchus mykiss (rainbow trout)  
Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 619)  
Govoroun, M., Guiguen, Y. and Le Gac, F.  
Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss  
Unpublished (2003)  
On Dec 17, 2003 this sequence version replaced gi:39992052.  
Contact: Guiguen Y  
INRA - SCRIBE  
Campus de beaulieu, RENNES cedex, 35042, France  
Tel: 02.23.48.50.09  
Fax: 02.23.48.50.20  
Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us at [sigenasupport@jouy.inra.fr](mailto:sigenasupport@jouy.inra.fr) to obtain the chromatogram of this sequence.  
Plate: 0027 row: 1 column: 14  
Seq primer: M13R.

**JOURNAL**  
COMMENT

**FEATURES**  
Source  
1..619  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/db\_xref="taxon:8022"  
/clone="tcdk0027c.1.14"  
/cissue\_type="multi-issues"  
/dev\_stage="from embryos to adults"  
/lab\_host="DH10B"  
/clone\_lib="tcdk"

/note="Vector: pT73D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction; Clone distribution : AGENAE Resource centre, Francois Piumi, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

## ORIGIN

Query Match 83.2%; Score 20.8; DB 5; Length 619;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGCAGACTCTCTAC 25  
Db 619 CTTGTGATCCAGTACACTCTCTAC 596

## RESULT 13

CA052009 623 bp mRNA linear EST 04-MAR-2003  
LOCUS ssalrpb531310 mixed\_tissue Salmo salar cDNA, mRNA sequence.  
DEFINITION CA052009  
VERSION CA052009.1 GI:24382252  
KEYWORDS EST.  
SOURCE Salmo salar (Atlantic salmon)

ORGANISM Salmo salar  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Proacanthopterygii; Salmoniformes; Salmonidae; Salmo.

## REFERENCE

AUTHORS GRASP Consortium, Davidson, W.S., Koop, B.F. and  
TITLE http://web.uvic.ca/cbr/grasp.  
JOURNAL A survey of Salmo salar transcripts from high complexity cDNA  
COMMENT libraries  
Unpublished (2002)

## JOURNAL

## COMMENT

Contact: Koop BF  
Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Genome Sciences Centre, BC Cancer Agency  
cDNA preparation, sequencing and bioinformatics:  
Y Butterfield, R Kirkpatrick, J Asano, N Ginn, R Guin, D Lee,  
S Lee, T Olson, P Pandoh, A Prabh, D Smalhus, L Spence, J Stott,  
S Taylor, G Yang, J Schein, S Jones and M Marra.  
Location/Qualifiers

## FEATURES

## source

1..623  
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/mol\_type="mRNA"  
/strain="McConnell"  
/db\_xref="taxon:8030"  
/clone\_lib="mixed\_tissue"  
/note="Vector: pCWSport6; Library Creator: Research Genetics; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seagrass Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

## ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 623;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGCAGACTCTCTAC 25  
Db 558 CTTGTGATCCAGTACACTCTCTAC 581

## RESULT 14

CR369095/c

LOCUS CR369095 642 bp mRNA linear EST 21-APR-2004  
DEFINITION CR369095 AGENAE Rainbow trout normalized testis library (tcbl)  
ONCORHYNCHUS MYKISS cDNA clone tcbl0021c.n.22 5prim, mRNA sequence.  
ACCESSION CR369095  
VERSION CR369095.1 GI:46480407  
KEYWORDS EST.  
SOURCE Oncorhynchus mykiss (rainbow trout)

## ORIGIN

Query Match 83.2%; Score 20.8; DB 7; Length 642;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGCAGACTCTCTAC 25  
Db 472 CTTGTGATCCAGTACACTCTCTAC 449

## ORIGIN

Query Match 83.2%; Score 20.8; DB 7; Length 642;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## FEATURES

## source

1..642  
Location/Qualifiers  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
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/tissue\_type="testis"  
/lab\_host="RDH10B"  
/clone\_lib="AGENAE Rainbow trout normalized testis library (tcbl)"  
/note="Vector: pT73D-pac; Clone distribution : AGENAE Resource centre, Francois Piumi, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

## ORIGIN

Query Match 83.2%; Score 20.8; DB 7; Length 642;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGCAGACTCTCTAC 25  
Db 472 CTTGTGATCCAGTACACTCTCTAC 449

## RESULT 15

CB507124 657 bp mRNA linear EST 16-MAY-2003  
LOCUS ssalrpb50534 reproductive Salmo salar cDNA, mRNA sequence.  
DEFINITION CB507124  
VERSION CB507124.1 GI:29318770  
KEYWORDS EST.

## ORIGIN

Query Match 83.2%; Score 20.8; DB 7; Length 642;  
Best Local Similarity 91.7%; Pred. No. 56;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGCAGACTCTCTAC 25  
Db 472 CTTGTGATCCAGTACACTCTCTAC 449

## RESULT 16

CR369095/c

Centre for Biomedical Research  
 University of Victoria  
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
 Tel: 250 472 4067  
 Fax: 250 472 4075  
 Email: bkcorp@vic.ca  
 Genome Sciences Centre, BC Cancer Agency CDNA preparation,  
 sequencing and bioinformatics: Y Buterfield, R Kirkpatrick, J  
 Amano, N Guin, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D  
 Smalhus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and  
 M Marra.

## POLYMER

## FEATURES

## SOURCE

## Location/Qualifiers

1. .657  
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 /mol\_type="mRNA"  
 /strain="McConnell"  
 /db\_xref="taxon:8330"  
 /clone\_id="reproductive"  
 /note="Vector: pBluescriptISK+; Library Creator:  
 Kristian R von Schalburg; Atlantic salmon tissue  
 contributors: Carlo Biagi, Mitch Un and Robert Devlin  
 (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.),  
 Seapring Hatchery (Crofton, B.C.), Rachel Roper  
 (University of Victoria)"

## ORIGIN

## Query Match

83.2%; Score 20.8; DB 6; Length 657;

Best Local Similarity 91.7%; Pred. No. 56;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGGACACTCTAC 25

DB 433 CTTGTGATCCAGGATCACTCTAC 456

Search completed: February 9, 2005, 21:55:48  
 Job time : 2451.85 secs

